

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 9, 2005, 23:46:53 ; Search time 40 Seconds
 (without alignments)
 921.276 Million cell updates/sec

Title: US-10-056-405-2
 Perfect score: 383
 Sequence: 1 MVYNFKVFKKCAPNGKVTLY.....ADVETFRQDTIDQQASVDFE 383

Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	20	5.2	364 2	A34867 arrestin - fruit fly (Drosophila melanogaster)
2	17	4.4	363 2	C;Species: Drosophila melanogaster C;Accession: A34867; A34868 R;Smith, D.P.; Shieh, B.H.; Zuker, C.S.
3	16	4.2	381 2	B56607 arrestin homolog -
4	12	3.1	407 2	A56607 arrestin homolog -
5	11	2.9	401 2	A34865 49K photoreceptor arrestin homolog -
6	11	2.9	401 2	S11566 arrestin 2 - blueb arrestin isoform 2
7	11	2.9	401 2	B55081 arrestin isoform 2
8	11	2.9	405 2	S68254 arrestin isoform 1
9	11	2.9	407 2	S68253 arrestin - human (
10	11	2.9	409 2	S18984 arrestin - human (
11	11	2.9	410 2	A59279 beta-arrestin 2 - arrestin isoform 1
12	11	2.9	415 2	S68255 arrestin arrJU - b
13	11	2.9	420 2	A47140 arrestin-C - human
14	9	2.3	387 2	I55423 arrestin - human
15	9	2.3	388 2	S38943 hypothetical prote S-antigen - mouse
16	9	2.3	1773 2	T05128 S-antigen - rat
17	8	2.1	403 2	J80066 S-antigen - bovine
18	8	2.1	403 2	S03960 retinal S-antigen
19	8	2.1	404 2	A28404 DNA/pantothenate m
20	8	2.1	405 2	A30357 beta-arrestin 1, s
21	8	2.1	412 2	F87709 beta-arrestin, bra
22	8	2.1	418 2	B46682 beta-arrestin - r
23	8	2.1	418 2	A34851 beta-arrestin, bra
24	8	2.1	418 2	B43404 probable signal re
25	8	2.1	448 2	D71852 signal recognition
26	8	1.8	448 2	H64663 nitrogen fixation
27	7	1.8	53 2	AF2764 protein-tyrosine k
28	7	1.8	57 2	PT0202 E5 protein - human
29	7	1.8	83 1	W5WLHS A;Molecule type: mRNA

RESULT 1

A34867
arrestin - fruit fly (Drosophila melanogaster)

C;Species: Drosophila melanogaster
C;Accession: A34867; A34868
R;Smith, D.P.; Shieh, B.H.; Zuker, C.S.

Proc. Natl. Acad. Sci. U.S.A. 87, 1003-1007, 1990

A;Title: Isolation and structure of an arrestin gene from Drosophila.

A;Reference number: A34867; MUID:90138925; PMID:1689056

A;Accession: A34867
A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-364 <SMI>

A;Cross-references: UNIPROT:P15372; GB:M30177
R;Hyde, D.R.; Mecklenburg, K.L.; Pollock, J.A.; Vihtelic, T.S.; Benzer, S.

Proc. Natl. Acad. Sci. U.S.A. 87, 1008-1012, 1990

A;Title: Twenty Drosophila visual system cDNA clones: one is a homolog of human arrestin

A;Reference number: A34868; MUID:90138926; PMID:2105491

A;Accession: A34868
A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-364 <HYD>

A;Cross-references: GB:M30140; NID:g156961; PIDN:AAA28380.1; PID:g156962
C;Genetics:

A;Gene: FlyBase:Arr1

A;Cross-references: FlyBase:FBgn0000120
A;Introns: 36/3; 30/3; 34/3
C;Superfamily: arrestin

Query Match 5.2%; Score 20; DB 2; Length 364;
Best Local Similarity 100.0%; Pred. No. 3e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY ||||||| ||||||| ||||| ||||| |||||
Db 227 VKKIKAMVQQGVDFVLFQNG 246

ALIGNMENTS

30	7	1.8	92 2	B82603 hypothetical prote
31	7	1.8	111 2	S10222 hypothetical prote
32	7	1.8	139 2	B97426 flagellar basal-bo
33	7	1.8	139 2	AE2644 conserved hypothet
34	7	1.8	142 2	F81048 hypothetical prote
35	7	1.8	145 2	C64447 hypothetical prote
36	7	1.8	149 2	A87346 osmotically induci
37	7	1.8	151 2	A83639 hypothetical prote
38	7	1.8	155 2	C81827 allophycocyanin al
39	7	1.8	161 2	A27873 hypothetical prote
40	7	1.8	166 2	A95969 carQ protein - Myx
41	7	1.8	174 2	S39877 glycoprotein S - p
42	7	1.8	216 2	A61259 hypothetical prote
43	7	1.8	217 2	B64080 probable lipoprote
44	7	1.8	231 2	S73469 MTA/SAH nucleosida
45	7	1.8	231 2	A82084 N

hypothetical prote
hypothetical prote
flagellar basal-bo
conserved hypothet
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
allophycocyanin al
hypothetical prote
carQ protein - Myx
glycoprotein S - p
hypothetical prote
probable lipoprote
MTA/SAH nucleosida

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Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : PIR_79:*

1: pir1:*

2: pir2:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
1	20	5.2	364	A34867
2	17	4.4	363	A55081
3	16	4.2	381	B55607
4	12	3.1	407	A55607
5	11	2.9	401	A34856
6	11	2.9	401	S11566
7	11	2.9	401	B55081
8	11	2.9	405	S68254
9	11	2.9	407	S68253
10	11	2.9	409	S18984
11	11	2.9	410	A59279
12	11	2.9	415	S68255
13	11	2.9	420	A47140
14	9	2.3	387	155423
15	9	2.3	388	S38943
16	9	2.3	1773	T05128
17	8	2.1	403	J50066
18	8	2.1	403	S03960
19	8	2.1	404	A28404
20	8	2.1	405	A3037
21	8	2.1	412	F87709
22	8	2.1	418	B46682
23	8	2.1	418	A34851
24	8	2.1	418	B43404
25	8	2.1	448	D71852
26	8	2.1	448	H64663
27	7	1.8	53	AF2764
28	7	1.8	57	PT0202
29	7	1.8	83	W5WLHS

SUMMARIES

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Maximum DB seq length: 2000000000
Post-processing: Listing first 45 summaries
Database : PIR 79:
1: pir1:
2: pir2:
3: pir3:
4: pir4:

Title: US-10-056-405-2
Perfect score: 383
Sequence: 1 M V Y N F T K V F K K C A P N G K V T L Y A D V E T F R Q D T I D Q Q A S V D F E 383
Scoring table: OLIGO
Gapop 60.0 , **Gapext** 60.0
Searched: 283416 seqs, 96216763 residues
Word size : 0
Total number of hits satisfying chosen parameters: 283416

23

hypothetical prote
hypothetical prote
flagellar basal-bo
flagellar basal-bo
conserved hypothet
hypothetical prote
hypothetical prote
osmotically induci
hypothetical prote
allophycocyanin al
hypothetical prote
caro protein - Myx
glycoprotein S - p
hypothetical prote
probable lipoprote
MTA / SAH nucleosida

RESULT
A34867

number of hits satisfying chosen parameters: 283416

shed: 283416 seqs, 96216763 residues
size : 0

ng table: OLIGO Gapop 60.0 , Gapext 60.0

3:
act score:
ancc:
US-10-056-405-2
383
1 MVYNFKVKKCCAPNGKVTLY.....ADVENTFRODTIDQQASVDFE 383

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1	20	5.2	364	2	A34867	A;Residues: 1-364 <HYD>
2	17	4.4	363	2	A55081	A;Cross-references: GB:M30140; NID:g156961; PIDN:AAA28380.1; PID:g156962
3	16	4.2	381	2	B56607	C;Genetics:
4	12	3.1	407	2	A56607	A;Gene: FlyBase:Arr1
5	11	2.9	401	2	A34856	A;Cross-references: FlyBase:FBgn0000120
6	11	2.9	401	2	S11566	A;Introns: 36/3; 306/3; 349/3
7	11	2.9	401	2	B55081	C;Superfamily: arrestin
8	11	2.9	405	2	S68254	arrestin - fruit fly
9	11	2.9	407	2	S68253	arrestin 1 - bluebottle fly
10	11	2.9	409	2	S18984	arrestin homolog - arrestin 1 - human
11	11	2.9	410	2	A59279	arrestin isoform 1 - human
12	11	2.9	415	2	S68255	arrestin isoform 1 - human
13	11	2.9	420	2	A47140	arrestin arr3L - bovine
14	9	2.3	387	2	155423	arrestin-C - human
15	9	2.3	388	2	S38943	arrestin - human
16	9	2.3	1773	2	T05128	hypothetical protein - human
17	8	2.1	403	2	J50066	S-antigen - mouse
18	8	2.1	403	2	S03960	S-antigen - rat
19	8	2.1	404	2	A28404	S-antigen - bovine
20	8	2.1	405	2	A30357	retinal S-antigen - bovine
21	8	2.1	412	2	F87709	DNA/pantothenate kinase - bovine
22	8	2.1	418	2	B46682	beta-arrestin 1 - bovine
23	8	2.1	418	2	A34851	beta-arrestin 1 - bovine
24	8	2.1	418	2	B433404	beta-arrestin 1 - bovine
25	8	2.1	448	2	D71852	probable signal recognition protein - bovine
26	8	2.1	448	2	H64663	nitrogen fixation protein - bovine
27	1	1.8	53	2	AF2764	protein-tyrosine kinase - bovine
28	7	1.8	57	2	PT0202	PTEN - bovine
29	1	1.8	83	1	W5WTHS	W5WTHS - bovine

A;Residues: 1-363 <PLA>
 A;Cross-references: UNIPROT:PS1486; GB:X79072; NID:9483527; PIDN:CAA55672.1; PID:9483528
 A;Note: the source is designated as Calliphora erythrocephala
 C;Superfamily: arrestin

Query Match
 Best Local Similarity 4.4%; Score 17; DB 2; Length 363;
 Matches 17; Conservative 0; Pred. No. 3.8e-09; Mismatches 0; Indels 0; Gaps 0;
 QY 322 SYAVKVVKLPGALGGE 338
 DB 321 SYAVKVVKLPGALGGE 337

RESULT 3
 B56607
 arrestin homolog - tobacco budworm
 C;Species: Heliothis virescens (tobacco budworm)
 C;Accession: B56607
 R;Raming, K.; Freitag, J.; Krieger, J.; Breer, H.
 Cell. Signal. 5, 69-80, 1993
 A;Title: Arrestin-subtypes in insect antennae.
 A;Reference number: A56607; MUID:9319955; PMID:8452755
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-381 <RAM>
 A;Cross-references: UNIPROT:P55274
 A;Experimental source: antennae
 C;Superfamily: arrestin

Query Match
 Best Local Similarity 4.4%; Score 17; DB 2; Length 363;
 Matches 17; Conservative 0; Pred. No. 3.8e-09; Mismatches 0; Indels 0; Gaps 0;
 QY 322 SYAVKVVKLPGALGGE 338
 DB 321 SYAVKVVKLPGALGGE 337

RESULT 3
 B56607
 arrestin homolog - tobacco budworm
 C;Species: Heliothis virescens (tobacco budworm)
 C;Accession: B56607
 R;Raming, K.; Freitag, J.; Krieger, J.; Breer, H.
 Cell. Signal. 5, 69-80, 1993
 A;Title: Arrestin-subtypes in insect antennae.
 A;Reference number: A56607; MUID:9319955; PMID:8452755
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-401 <YAM>
 A;Cross-references: UNIPROT:P19107; GB:M32141; NID:9158157; PIDN:AAA28833.1; PID:91581
 A;Gene: FlyBase:Arr2
 C;Superfamily: arrestin

Query Match
 Best Local Similarity 2.9%; Score 11; DB 2; Length 401;
 Matches 11; Conservative 0; Pred. No. 0.0067; Mismatches 0; Indels 0; Gaps 0;
 QY 62 RYGRGEEDEVMG 72
 DB 61 RYGRGEEDEVMG 71

RESULT 6
 S11566
 arrestin homolog - fruit fly (Drosophila miranda)
 C;Species: Drosophila miranda
 C;Accession: S11566
 R;Krishnan, R.; Ganguly, R.
 A;Title: Nucleic Acids Res. 18, 5894, 1990
 A;Reference number: S11566; MUID:91016944; PMID:2216789
 A;Accession: S11566; MUID:91016944; PMID:2216789
 A;Status: preliminary; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-401 <KRI>
 A;Cross-references: UNIPROT:P19108; EMBL:X54084; NID:97612; PIDN:CAA38019.1; PID:9295739
 A;Gene: FlyBase:Dmir/Arr2
 A;Cross-references: FlyBase:FBgn0012552
 C;Superfamily: arrestin

Query Match
 Best Local Similarity 2.9%; Score 11; DB 2; Length 401;
 Matches 11; Conservative 0; Pred. No. 0.0067; Mismatches 0; Indels 0; Gaps 0;
 QY 62 RYGRGEEDEVMG 72
 DB 61 RYGRGEEDEVMG 71

RESULT 6
 S11566
 arrestin homolog - fruit fly (Drosophila miranda)
 C;Species: Drosophila miranda
 C;Accession: S11566
 R;Krishnan, R.; Ganguly, R.
 A;Title: Nucleic Acids Res. 18, 5894, 1990
 A;Reference number: S11566; MUID:91016944; PMID:2216789
 A;Accession: S11566; MUID:91016944; PMID:2216789
 A;Status: preliminary; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-401 <KRI>
 A;Cross-references: UNIPROT:P19108; EMBL:X54084; NID:97612; PIDN:CAA38019.1; PID:9295739
 A;Gene: FlyBase:Dmir/Arr2
 A;Cross-references: FlyBase:FBgn0012552
 C;Superfamily: arrestin

Query Match
 Best Local Similarity 3.1%; Score 12; DB 2; Length 407;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 62 RYGRGEEDEVMGL 73
 DB 69 RYGRGEEDEVMGL 80

RESULT 7
 B55081
 arrestin 2 - bluebottle fly (Calliphora vicina)
 C;Species: Calliphora vicina
 C;Accession: B55081; S44292
 R;Plangger, A.; Malicki, D.; Whitney, M.; Paulsen, R.
 J. Biol. Chem. 269, 26969-26975, 1994
 A;Title: Mechanism of arrestin 2 function in rhabdomeric photoreceptors.
 A;Reference number: A55081; MUID:95014564; PMID:7929436
 A;Accession: B55081
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-401 <PLA>
 A;Cross-references: UNIPROT:PS1487; EMBL:X79073; NID:9483583; PIDN:CAA55673.1; PID:948356

Query Match
 Best Local Similarity 100.0%; Score 12; DB 2; Length 407;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 62 RYGRGEEDEVMGL 73
 DB 69 RYGRGEEDEVMGL 80

RESULT 5
 A34856
 49K photoreceptor protein - fruit fly (Drosophila melanogaster)
 C;Superfamily: arrestin

Query Match 2.9%; Score 11; DB 2; Length 401;
 Best Local Similarity 100.0%; Pred. No. 0.0057;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 C;Superfamily: arrestin

Qy 62 RYGREDEVMG 72
 Db 61 RYGREDEVMG 71

RESULT 8

S68254 arrestin isoform 2S, erythrocyte - rainbow trout
 C;Species: *Oncorhynchus mykiss* (rainbow trout)
 C;Accession: S68254
 C;Date: 06-Dec-1995 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 R;Jahns, R.; Borgee, F.; Lindenthal, S.; Straub, A.; Motaia, R.; Fievet, B.
 Biochem. J. 316, 497-506, 1996
 A;Title: Trout red blood cell arrestin (TRCarr), a novel member of the arrestin family:
 A;Reference number: S68253; MUID:96257743; PMID:8687393
 A;Accession: S68254
 A;Status: Preliminary; nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-405 <JAH>
 A;Cross-references: UNIPROT:P51467; GB:U48410
 C;Superfamily: arrestin

Query Match 2.9%; Score 11; DB 2; Length 405;
 Best Local Similarity 100.0%; Pred. No. 0.0068;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 341 ELPFVLMHPKP 351
 Db 339 ELPFVLMHPKP 349

RESULT 9

S68253 arrestin isoform 1S, erythrocyte - rainbow trout
 C;Species: *Oncorhynchus mykiss* (rainbow trout)
 C;Accession: S68253
 C;Date: 06-Dec-1995 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 R;Jahns, R.; Borgee, F.; Lindenthal, S.; Straub, A.; Motaia, R.; Fievet, B.
 Biochem. J. 316, 497-506, 1996
 A;Title: Trout red blood cell arrestin (TRCarr), a novel member of the arrestin family:
 A;Reference number: S68253; MUID:96257743; PMID:8687393
 A;Status: Preliminary; nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-407 <JAH>
 A;Cross-references: UNIPROT:P51466; GB:U48410; NID:91215723; PIDN:AAB16954.1; PID:912157
 C;Superfamily: arrestin

Query Match 2.9%; Score 11; DB 2; Length 407;
 Best Local Similarity 100.0%; Pred. No. 0.0068;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 341 ELPFVLMHPKP 351
 Db 339 ELPFVLMHPKP 349

RESULT 10

S18984 arrestin - human (fragment)
 C;Species: *Homo sapiens* (man)
 C;Accession: S18984
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
 R;Rapoport, B.
 R;Jahns, R.; Borgee, F.; Lindenthal, S.; Straub, A.; Motaia, R.; Fievet, B.
 Biochem. J. 316, 497-506, 1996
 A;Title: Trout red blood cell arrestin (TRCarr), a novel member of the arrestin family:
 A;Description: Isolation of a novel cDNA belonging to the arrestin family from human thy
 A;Reference number: S18984
 A;Accession: S18984

Query Match 2.9%; Score 11; DB 2; Length 409;
 Best Local Similarity 100.0%; Pred. No. 0.0068;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 341 ELPFVLMHPKP 351
 Db 340 ELPFVLMHPKP 350

RESULT 12

S68255 arrestin isoform 1L, erythrocyte - rainbow trout
 C;Species: *Oncorhynchus mykiss* (rainbow trout)
 C;Accession: S68255
 C;Date: 06-Dec-1995 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 R;Jahns, R.; Borgee, F.; Lindenthal, S.; Straub, A.; Motaia, R.; Fievet, B.
 Biochem. J. 316, 497-506, 1996
 A;Title: Trout red blood cell arrestin (TRCarr), a novel member of the arrestin family:
 A;Reference number: S68253; MUID:96257743; PMID:8687393
 A;Accession: S68255
 A;Status: Preliminary; nucleic acid sequence not shown

Page 4

A;Molecule type: mRNA
 A;Residues: 1-415 <JAH>
 C;Superfamily: arrestin
 Query Match
 Best Local Similarity 2.9%; Score 11; DB 2; Length 415;
 Matches 11; Conservative 100.0%; Pred. No. 0.0069; Mismatches 0; Indels 0; Gaps 0;
 Qy 341 ELPFVLMHPKP 351
 Db 347 ELPFVLMHPKP 357
 RESULT 13
 arrestin arr3L - bovine
 N-Contains: arrestin arr3S
 Species: Bos primigenius taurus (cattle)
 Date: 16-Feb-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
 ;Accession: A47140; B47140; JC2051
 ;Sterne-Marr, R.; Gurevich, V.V.; Goldsmith, P.; Bodine, R.C.; Sanders, C.; Donoso, L.A.
 ;Title: Polypeptide variants of beta-arrestin and arrestin3.
 ;Reference number: A47140; MUID:93340166; PMID:8340388
 Molecule type: mRNA
 Residues: 1-420 <STE>
 Cross-references: UNIPROT:P32120; GB:L14641
 Experimental source: brain
 Note: sequence extracted from NCBI backbone (NCBIn:136006, NCBIPI:136007)
 Molecule type: mRNA
 Residues: 1-362,374-420 <ST2>
 Comment: This protein plays a role in the regulation of G-protein-coupled receptors.
 Superfamily: arrestin
 -420/Product: arrestin arr3L #status predicted <MAT>
 -362,374-420/Product: arrestin arr3S #status predicted <MA2>
 Every Match
 best Local Similarity 2.9%; Score 11; DB 2; Length 420;
 matches 11; Conservative 100.0%; Pred. No. 0.007; Mismatches 0; Indels 0; Gaps 0;
 341 ELPFVLMHPKP 351
 339 ELPFVLMHPKP 349
 LT 14
 23
 arrestin-C - human
 species: Homo sapiens (man)
 : 24-May-1996 #sequence_revision 24-May-1996 #text_change 13-Sep-1998
 : C.M.; Whitmore, D.H.; Wiechmann, A.F.
 : Chem. 269, 4613-4619, 1994
 : Cone arrestin identified by targeting expression of a functional family.
 : number: 155423; MUID:94140898; PMID:8308033
 : preliminary; translated from GB/EMBL/DDBJ
 : due: 1-387 <RES>
 : references: EMBL:U03626; NID:9458200; PID:9458201
 Y Match
 Local Similarity 2.3%; Score 9; DB 2; Length 387;
 matches 9; Conservative 0; Pred. No. 0.76; Mismatches 0; Indels 0; Gaps 0;
 22 GKRDFVHDY 30
 19 GKRDFVHDY 27
 RESULT 15
 S38943
 arrestin - human
 C:Species: Homo sapiens (man)
 C;Date: 19-May-1994 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
 C;Accession: S38943
 R;Murakami, A.; Yajima, T.; Sakuma, H.; McLaren, M.J.; Inana, G.
 FEB5 Lett. 334, 203-209, 1993
 A;Title: X-arrestin: a new retinal arrestin mapping to the X chromosome.
 A;Reference number: S38943; MUID:94039835; PMID:8224247
 A;Accession: S38943
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-388 <MUR>
 A;Cross-references: UNIPROT:P36575; GB:S66793; NID:9439830; PID:9439831
 C;Superfamily: arrestin
 Query Match
 Best Local Similarity 2.3%; Score 9; DB 2; Length 388;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 22 GKRDFVHDY 30
 Db 19 GKRDFVHDY 27
 Search completed: February 10, 2005, 00:02:18
 Job time : 42 secs

RESULT 2
A34867
arrestin - fruit fly (*Drosophila melanogaster*)
C;Species: *Drosophila melanogaster*
C;Accession: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 09-Jul-2004
R;Smith, D.P.; Shieh, B.H.; Zuker, C.S.
A;Title: Isolation and structure of an arrestin gene from *Drosophila*.
A;Reference number: A34867; MUID:90138925; PMID:1689056
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-364 <HVD>
A;Cross-references: UNIPROT:P51486; GB:X79072; NID:9483527; PIDN:CAA55672.1; PID:94
R; Hyde, D.R.; Mecklenburg, K.L.; Pollock, J.A.; Vihtelic, T.S.; Benzer, S.
A;Title: Twenty *Drosophila* visual system cDNA clones: one is a homolog of human arrestin
A;Accession: A34868; MUID:90138926; PMID:2105491
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-364 <HVD>
C;Genetics: A;Gene: FlyBase:Arr1
A;Cross-references: FlyBase:FBgn0000120
A;Introns: 36/3; 306/3; 349/3
C;Superfamily: arrestin

Query Match
Best Local Similarity 70.1%; Score 1384; DB 2; Length 363;
Matches 258; Conservative 51; Mismatches 55; Indels 8; Gaps 2;
Qy 1 MVYNFKVKFKCAPNGKVTLYMGRDFVDHVGVEPIDGIVWLDEYIRDNRKVFGQIVCS 60
Db 1 MVYNFKVKFKCAPNGKVTLYMGRDFVDHVGVEPIDGIVWLDEYIRDNRKVFGQIVCS 60
Qy 61 FRYGREDDEVMGLNFQKELCLASEQIYPRPEKSDEQKTLQERLKKLGSNAIPFTNIS 120
Db 61 FRYGREDDEVMGLNFQKELCLASEQIYPRPEKSDEQKTLQERLKKLGSNAIPFTNIS 120
Qy 121 PNAPSSVTIQLQGEDDNGDPGCVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKOGO 180
Db 120 PSSPASVVLQQLQKANDSTQPGVQYFVKVAGENDCDRSHRRSTVNLGIRKVOYAPTKOGO 180
Qy 181 QPCTLVRKDFMLSPGELELEVTLDKQYHGERIGNICIRNNNSKVKIKAMVQGVD 179
Db 180 QPCTLVRKDFMLSPGELELEVTLDKQYHGERISKINICIRNNNSKVKIKAMVQGVD 179
Qy 241 VVLFONGSYRNTVASLETSEGCPPIQPGSSLLQKVMYLTPLLSNKQRGGIALDQIKRQDQ 239
Db 241 VVLFONGSYRNTVASLETSEGCPPIQPGSSLLQKVMYLTPLLSNKQRGGIALDQIKRQDQ 239
Qy 301 CLASTTLAQPORDQDAFGVIIYAVVKVLFLGALGGEESAELPPVIMHPKPGTKAVTHA 360
Db 300 SLASTTLIASQEARDAAFGIIVSYAVVKVLFLGALGGECAELPPVIMHPKPGTKAVTHA 360
Qy 361 DSQADVET 368
Db 355 --QPEAET 360

RESULT 4
A56607
arrestin homolog - migratory locust
C;Species: *Locusta migratoria* (migratory locust)
C;Accession: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004
R;Raming, K.; Freilag, J.; Krieger, J.; Breer, H.
A;Title: Arrestin-subtypes in insect antennae
A;Reference number: A56607; MUID:93199955; PMID:8452755
A;Contents: antennae
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-407 <RAM>
A;Cross-references: UNIPROT:P32122; GB:S57174; NID:9298755; PIDN:AAB25860.1; PID:9298756
C;Superfamily: arrestin

Query Match
Best Local Similarity 50.4%; Score 993.5; DB 2; Length 407;
Matches 202; Conservative 64; Mismatches 107; Indels 15; Gaps 8;
Qy 6 KVFKVKCAPNGKVTLYMGRDFVDHVGVEPIDGIVWLDEYIRDNRKVFGQIVCS 65
Db 14 KVFKVKCAPNGKVTLYMGRDFVDHVGVEPIDGIVWLDEYIRDNRKVFGQIVCS 65
Qy 66 EDEEVMLNQKELCLASEQIYPRPEKSDEQKTLQERLKKLGSNAIPFTNIS 125
Db 73 EDEEVMLNQKELCLASEQIYPRPEKSDEQKTLQERLKKLGSNAIPFTNIS 125
Qy 126 SVTLQQGEDDNGDPGCVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKOGO-PCT 131

Query Match
Best Local Similarity 52.1%; Score 993.5; DB 2; Length 407;
Matches 202; Conservative 64; Mismatches 107; Indels 15; Gaps 8;
Qy 6 KVFKVKCAPNGKVTLYMGRDFVDHVGVEPIDGIVWLDEYIRDNRKVFGQIVCS 65
Db 14 KVFKVKCAPNGKVTLYMGRDFVDHVGVEPIDGIVWLDEYIRDNRKVFGQIVCS 65
Qy 66 EDEEVMLNQKELCLASEQIYPRPEKSDEQKTLQERLKKLGSNAIPFTNIS 125
Db 73 EDEEVMLNQKELCLASEQIYPRPEKSDEQKTLQERLKKLGSNAIPFTNIS 125
Qy 126 SVTLQQGEDDNGDPGCVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKOGO-PCT 131

Best Local Similarity 47.8%; Pred. No. 2e-67; Matches 187; Conservative 70; Mismatches 122; Indels 13; Gaps 6;

Qy

1 MVNFFKVKCARNKVTLYMGRDFVDRHVGVEPIDGIVLVDDEYIRDRKVFQIVCS

Db

1 MVVSVKVKFVKATPNKGKVTYFLGRHFDYIDPVGIVVDPDVK-NRKVEAQLATI 59

Qy

61 FRYGREDEEVMLNQKELCLASEOIQYPREPKSDKEQTKLQERLKKLGNSNAPTFNIS 120

Db

60 YRYGREDEEVMGVKFESKELCLICRQEVIM-GNSNNMEMPTQEKLVKLGNSNAHPTFHFP 118

Qy

121 PNAPSSTLQGEDDNGDPCGVSYVKIFAGSESETDRTHRSTVTLGIRKIQAPTKQGQOPCTL 185

Db

119 PNSPSSVTLOQEGDDLGKPLGVETIRAYVADSEDDRQHRSMSVSLVKKLQYAPPTRQ 178

Qy

181 Q-PCTLVRKDFMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKMKKIKAMVQGVDVLFQ 245

Db

179 RLPSLIVSKGFTFSNGKISLBEVTLREYVHGEKRYATVQINNSKKAVKNIKVFIQHT 238

Qy

240 DVVLFQNGSYRNTVASLETSEGCPICQPGSSLQKVMYLTPLLSSNKKQRGIALDGOIKRQOCLAST 305

Db

239 EITMV-NAQFSKHKVQALETKEGCPITPGANLSTKTFYLIPLASNNSKDRHGTALDGHKDED 297

Qy

300 QCLASTLILAQ-PDQDRAFTGVLISYAVKVKLFLGALGELSAELPFVLMHPPGKTRQD 299

Db

298 VNLASSTMVQDGKSTGACGIVLISYVRKLNCGTUGETQDVFVFKLQAPGSVEKKR 357

Qy

354 ---KAKVHADSOADVENTFROTDIDQASVDF 382

Db

358 SNAMKKMKSIQHRNTQGYQDDDDNIVFEDF 389

RESULT 8

Qy

Db

Best Local Similarity 45.8%; Score 903.5; DB 2; Length 418; Matches 178; Conservative 46.8%; Pred. No. 2.8e-64; Mismatches 78; Indels 11; Gaps 5;

Qy

6 KVFKKCAPNGKVTLYMGRDFVDRHVGVEPIDGIVLVDDEYIRDRKVFQIVCSFRYGR 65

Db

7 RVFKKASPNQKLTLYMGRDFVDRHIDLVDPGVVLVDPPEYLKE-RRVYVLTCAFRYGR 65

Qy

6 EDEVMGLNQKELCLASEOIQYPREPKSDKEQTKLQERLKKLGNSNAPTFNISPNARS 125

Db

66 EDLVDVGLTFRKDLFVANVQSPAPEDKKPLTRLQERLKKLGNSNAPTFNISPNARS 125

Qy

126 SVTLQGQEDDNGDPCGVSYVKIFAGSESETDRTHRSTVTLGIRKIQAPTKQGOQOPCTL 185

Db

126 SVTLQPGPDTGKACGIVYEVKAPCALENLEEKIHKKNSVRLVKQYAPERPGPQPTAE 185

Qy

186 VRKDFMSRSGELELEVTLDKOLYLHGERIGVNICIRNNSNKMKKIKAMVQGVDVLFQ 245

Db

186 ITROPLMSDKPLHLEASLDKEIYHGEPISVNHWHTNTKTKKIKSYROYADICLEN 245

Qy

246 TAQYKCPVAMEADD-TVAPSSTFCVYLTPEFLANRREKGLALDGKLKHEDTNLASS 303

Db

304 TLLAQPQDRAFTGVLISYAVKVKLFL--GALGGELSA---ELPFVLMHPPGKTR-A 355

Qy

356 KVTHADSOADVENTFROTDIDQASVDF 375

Db

364 EVPESETPVDTNILEDND 383

Query Match

Best Local Similarity 45.8%; Score 903.5; DB 2; Length 418; Matches 179; Conservative 47.1%; Pred. No. 2.8e-64; Mismatches 76; Indels 112; Gaps 5;

Qy

6 KVFKKCAPNGKVTLYMGRDFVDRHVGVEPIDGIVLVDDEYIRDRKVFQIVCSFRYGR 65

Db

7 RVFKKASPNQKLTLYMGRDFVDRHIDLVDPGVVLVDPPEYLKE-RRVYVLTCAFRYGR 65

Qy

66 EDEVMGLNQKELCLASEOIQYPREPKSDKEQTKLQERLKKLGNSNAPTFNISPNARS 125

Db

66 EDLVDVGLTFRKDLFVANVQSPAPEDKKPLTRLQERLKKLGNSNAPTFNISPNARS 125

Qy

356 KVTHADSOADVENTFROTDIDQASVDF 375

Db

364 EVPESETPVDTNILEDND 383

RESULT 10

B46682

A;Species: Homo sapiens (man)

C;Species: Bos primigenius taurus (cattle)

C;Date: 16-Feb-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004

C;Accession: A47140; B47140; JC2051

R;Sterne-Marr, R.; Gurevich, V.V.; Goldsmith, P.; Bodine, R.C.; Sanders, C.; Donoso, L.A.;Title: Polypeptide variants of beta-arrestin and arrestin3.

A;Reference number: A47140; MUID:93340166; PMID:8340388

A;Accession: A47140

A;Molecule type: mRNA

A;Residues: 1-420 <STE>

A;Cross-references: UNIPROT:P32120; GB:L14641

A;Experimental source: brain

A;Note: Sequence extracted from NCBI backbone (NCBIN:136006, NCBIPI:136007)

A;Accession: B47140

A;Molecule type: mRNA

A;Residues: 1-362,374-420 <ST2>

A;Note: This protein plays a role in the regulation of G-protein-coupled receptors.

C;Comment: This protein plays a role in the regulation of G-protein-coupled receptors.

C;Superfamily: arrestin

F;1-420/Product: arrestin arr3L #Status predicted <MAT>

F;1-362,374-420/Product: arrestin arr3L #Status predicted <MAT>

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-333,342-418 <PAR2>

A;Cross-references: GB:L04685; NID:g347956; PIDN:AAA35556.1; PID:g347957

A;Accession: A46682

A;Note: sequence extracted from NCBI backbone (NCBIPI:134015)

A;Genes: GDB:ARRB1; ARRI

A;Cross-references: GDB:141541; OMIM:107940

A;Map position: 11q13-11q13

C;Superfamily: arrestin

C;Keywords: alternative splicing

Query Match 45.2% Score 891.5; DB 2; Length 418; Best Local Similarity 46.3%; Pred. No. 2.5e-63; Matches 176; Conservative 78; Mismatches 113; Indels 13; Gaps 5;

Qy 6 KVFKKCAPNGKVTLYMGKRDFFDVHVGVEPIDGIVVLDEYIRDNRKVFQGIVCSFRYGR 65

Db 7 RVFKKSSPNCKLTVLGKRDFFDVHLDKVPDVGVVLVDPLKD-RKVFTLTCAFRYGR 66

Qy 66 EEDEVMLNFOKEKLCLASEQIYPRPEKSDKEOTKLOERLLKKLGSNAIPFTFNISPNA 125

Db 67 EDLVLGLSFRKDLFIANYQAFPPTPNPPRPPTRLQERLLRKQHAPFFFTIPQNLPC 126

Qy 126 SVTLQOGEDDNGDPCGVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGOOPCTL 185

Db 127 SVTLQPGPDETGKACGVDFEIRFCAKSLEEKSHKRNSVRLVIRKVQFAPEKPGPQPSAE 186

Qy 186 VRKDFMLSPGELEVLTDQKVLHGERIGVNICIRNNSNKMKVKKIKAMVQGVDVLFQ 245

Db 187 TTRHFLMSDRSLHLEASLDKELYHGPSPLNVNVTNNSTKTVKIKVSVROYADICLFS 246

Qy 246 NGSYRNTVASLETSEGCPQPGSSLQKVMYLTPLSSNKQRGGIALDQQIKRQDQCLAST 305

Db 247 TAQYKCPVAVQEODD--QVSPPSSTECKYTTPLSNNREKRGALDGKLIKEDTNLASS 304

Qy 306 TLLAQPDQDAFGVILISYAVKVKLFLGALGGELSAELPFLVMHPKP 351

Db 305 TIVKEGANKEVLGILVSYRVRVKLVV-SRGDDVSVELPFVLMHPKP 349

RESULT 11

A47140

arrestin arr3L - bovine

N;Contains: arrestin arr3S

C;Species: Bos primigenius taurus (cattle)

C;Date: 16-Feb-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004

C;Accession: A47140; B47140; JC2051

R;Sterne-Marr, R.; Gurevich, V.V.; Goldsmith, P.; Bodine, R.C.; Sanders, C.; Donoso, L.A.;Title: Polypeptide variants of beta-arrestin and arrestin3.

A;Reference number: A47140; MUID:93340166; PMID:8340388

A;Accession: A47140

A;Molecule type: mRNA

A;Residues: 1-420 <STE>

A;Cross-references: UNIPROT:P32120; GB:L14641

A;Experimental source: brain

A;Note: Sequence extracted from NCBI backbone (NCBIN:136006, NCBIPI:136007)

A;Accession: B47140

A;Molecule type: mRNA

A;Residues: 1-362,374-420 <ST2>

A;Note: This protein plays a role in the regulation of G-protein-coupled receptors.

C;Comment: This protein plays a role in the regulation of G-protein-coupled receptors.

C;Superfamily: arrestin

F;1-420/Product: arrestin arr3L #Status predicted <MAT>

F;1-362,374-420/Product: arrestin arr3L #Status predicted <MAT>

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-418 <PAR1>

A;Cross-references: UNIPROT:P49407; GB:L04685; PIDN:AAA35559.1; PID:g347958

A;Accession: A46682

A;Note: Sequence extracted from NCBI backbone (NCBIPI:134014)

A;Genes: GDB:ARRB1; ARRI

A;Cross-references: GDB:141541; OMIM:107940

A;Map position: 11q13-11q13

C;Keywords: alternative splicing

Query Match 45.0% Score 887; DB 2; Length 420; Best Local Similarity 48.3%; Pred. No. 5.8e-63; Matches 167; Conservative 78; Mismatches 97; Indels 4; Gaps 3;

Qy 6 KVFKKCAPNGKVTLYMGKRDFFDVHVGVEPIDGIVVLDEYIRDNRKVFQGIVCSFRYGR 65

Db 8 RVFKKSSPNCKLTVLGKRDFFDVHLDKVPDVGVVLVDPLKD-RKVFTLTCAFRYGR 66

Qy 126 SVTLQOGEDDNGDPCGVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGOOPCTL 185

Db 127 SVTLQPGPDETGKACGVDFEIRFCAKSLEEKSHKRNSVRLVIRKVQFAPEKPGPQPSAE 186

Qy 186 VRKDFMLSPGELEVLTDQKVLHGERIGVNICIRNNSNKMKVKKIKAMVQGVDVLFQ 245

Db 187 TTRHFLMSDRSLHLEASLDKELYHGPSPLNVNVTNNSTKTVKIKVSVROYADICLFS 246

Qy 246 NGSYRNTVASLETSEGCPQPGSSLQKVMYLTPLSSNKQRGGIALDQQIKRQDQCLAST 305

Db 247 TAQYKCPVAVQEODD--QVSPPSSTECKYTTPLSNNREKRGALDGKLIKEDTNLASS 304

Qy 306 TLLAQPDQDAFGVILISYAVKVKLFLGALGGELSAELPFLVMHPKP 351

Db 305 TIVKEGANKEVLGILVSYRVRVKLVV-SRGDDVSVELPFVLMHPKP 349

RESULT 12

S18984

arrestin - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C;Accession: S18984

R;Rapoport, B.

submitted to the EMBL Data Library, November 1991

A;Description: Isolation of a novel cDNA belonging to the arrestin family from human thy.

A;Reference number: S18984

A;Accession: S18984

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-409 <RAP>

A;Cross-references: UNIPROT:P32121; EMBL:Z11501; NID:g28850; PIDN:CAA77577.1; PID:g28851

C;Superfamily: arrestin

Query Match 44.7% Score 882; DB 2; Length 409; Best Local Similarity 48.3%; Pred. No. 1.4e-62; Matches 167; Conservative 76; Mismatches 99; Indels 4; Gaps 3;

Qy 6 KVFKKCAPNGKVTLYMGKRDFFDVHVGVEPIDGIVVLDEYIRDNRKVFQGIVCSFRYGR 65

Db 8 RVFKKSSPNCKLTVLGKRDFFDVHLDKVPDVGVVLVDPLKD-RKVFTLTCAFRYGR 66

Qy 66 EEDEVMLNFOKEKLCLASEQIYPRPEKSDKEOTKLOERLLKKLGSNAIPFTFNISPNA 125

Db 67 EDLVLGLSFRKDLFIATYQAFPPVNPFRPPTQDRLLRKQHAPFFFTIPQNLPC 126

QY 126 SVTLQOGEDDNGDPGVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQOPCTL 185
 Db 127 SVTLQGPEDTGKACCGVDFEIRACAKSIEBKSHKRNSVRVLRVKQFAPEKPGQPSAE 186
 QY 186 VRKDFMLSPGELEEVTLKDQKLQYLHGERIGVNICIRNNSNKMKKKIKAMVQOGVWLFQ 245
 Db 187 TTPHFLMSDRSLHIEASLDKELLYHGEPLNVNVHVTNNSTKTVKIKVSYROVADICLFS 246
 QY 246 NGSYRNTVASLETSEGCP1QPGSSLQKVMVLTPLISSNKORRGIAQIKRQDQCLAS 304
 Db 247 TAQYKCPVVAQLEQDD-QVSPSSTCKYVITIPLISDNREKRLGALDGKLKHEDTNLAS 305
 QY 305 TLLAQPDQDARFGVILSYAVKVKLFLGAGGELSAELPFLVMPKPG---TKAKVIIHAD 361
 Db 362 SQADVET---FQDIDQQAQSVDFE 363
 Db 364 SDPPIDTLLIREFEMNSQDDDFVFE 389

RESULT 13
 arrestin isoform 1S, erythrocyte - rainbow trout
 C;Species: *Oncorhynchus mykiss* (rainbow trout)
 C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 R;Jahns, R.; Borgese, F.; Lindenthal, S.; Straub, A.; Motais, R.; Pievet, B.
 Biochem. J. 316, 497-506, 1996
 A;Title: Trout red blood cell arrestin (TRCarr), a novel member of the arrestin family:
 A;Reference number: S68253; MUID:9625743; PMID:8687393
 A;Molecule type: mRNA
 A;Residues: 1-407 <JAH>
 A;Cross-references: UNIPROT:P51466; GB:U48410; NID:91215723; PIDN:AAH16954.1; PID:912157
 C;Superfamily: arrestin

Query Match
 Best Local Similarity 44.1%; Score 871; DB 2; Length 407;
 Matches 171; Conservative 82; Mismatches 121; Indels 12; Gaps 5;

QY 6 KVFKKCAPNGKVTLQMGKRDFTDHFVSGVERIDGIVVLVLDDEYIRDNRKVFGQIVCSFRYGR 65
 Db 8 RVFKKSSSPNCKVTLQMGKRDFTDHFVSGVERIDGIVVLVLDDEYIRDNRKVFGQIVCSFRYGR 65
 QY 66 EDEEVMLNFGQKELCLASEQIVPRPEKSDEQTKLQERLKKGSNAIPFTENISPNAPS 125
 Db 67 EDLDVIGLSFRKDLIATYQAFPPMPNPPRPPTRQLD-RKVFTVLTCAFRYGR 66
 QY 126 SVTLQOGEDDNGDPGVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQOPCTL 186
 Db 127 SVTLQGPEDTGKACCGVDFEIRACAKSIEBKSHKRNSVRVLRVKQFAPEKPGQPSAE 186
 QY 186 VRKDFMLSPGELEEVTLKDQKLQYLHGERIGVNICIRNNSNKMKKKIKAMVQOGVWLFQ 245
 Db 187 TTRHFLMSDRSLHIEASLDKELLYHGEPLNVNVHVTNNSTKTVKIKVSYROVADICLFS 246
 QY 246 NGSYRNTVASLETSEGCP1QPGSSLQKVMVLTPLISSNKORRGIAQIKRQDQCLAS 304
 Db 247 TAQYKCPVVAQLEQDD-QVSPSSTCKYVITIPLISDNREKRLGALDGKLKHEDTNLAS 305
 QY 305 TLLAQPDQDARFGVILSYAVKVKLFLGAGGELSAELPFLVMPKPG---TKAKVIIHAD 361
 Db 362 SQADVET---FQDIDQQAQSVDFE 363
 Db 364 SDPPIDTLLIREFEMNSQDDDFVFE 389

RESULT 14
 A59279 hypothetical protein F53H8.2 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000
 C;Accession: T34297
 R;Bradshaw, H.; Gattung, S.
 A;Description: The sequence of *C. elegans* cosmid F53H8.
 A;Reference number: Z21501
 A;Accession: T34297
 A;Status: preliminary; translated from GB/EMBL/DDBJ

RESULT 15
 A59279 beta-arrestin 2 - rat
 C;Species: *Rattus norvegicus* (Norway rat)
 C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
 C;Accession: A59279; A43404; T70112
 A;Status: preliminary; translated from GB/EMBL/DDBJ

Query Match
 Best Local Similarity 44.1%; Score 869.5; DB 2; Length 410;
 Matches 167; Conservative 76; Mismatches 99; Indels 5; Gaps 4;

QY 6 KVFKKCAPNGKVTLQMGKRDFTDHFVSGVERIDGIVVLVLDDEYIRDNRKVFGQIVCSFRYGR 65
 Db 8 RVFKKSSSPNCKVTLQMGKRDFTDHFVSGVERIDGIVVLVLDDEYIRDNRKVFGQIVCSFRYGR 65
 QY 66 EDEEVMLNFGQKELCLASEQIVPRPEKSDEQTKLQERLKKGSNAIPFTENISPNAPS 125
 Db 67 EDLDVIGLSFRKDLIATYQAFPPMPNPPRPPTRQLD-RKVFTVLTCAFRYGR 66
 QY 126 SVTLQOGEDDNGDPGVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQOPCTL 186
 Db 127 SVTLQGPEDTGKACCGVDFEIRACAKSIEBKSHKRNSVRVLRVKQFAPEKPGQPSAE 186
 QY 186 VRKDFMLSPGELEEVTLKDQKLQYLHGERIGVNICIRNNSNKMKKKIKAMVQOGVWLFQ 245
 Db 187 TTRHFLMSDRSLHIEASLDKELLYHGEPLNVNVHVTNNSTKTVKIKVSYROVADICLFS 246
 QY 246 NGSYRNTVASLETSEGCP1QPGSSLQKVMVLTPLISSNKORRGIAQIKRQDQCLAS 304
 Db 247 TAQYKCPVVAQLEQDD-QVSPSSTCKYVITIPLISDNREKRLGALDGKLKHEDTNLAS 305
 QY 305 TLLAQPDQDARFGVILSYAVKVKLFLGAGGELSAELPFLVMPKPG---TKAKVIIHAD 361
 Db 362 SQADVET---FQDIDQQAQSVDFE 363
 Db 364 SDPPIDTLLIREFEMNSQDDDFVFE 389

RESULT 15
 A59279 hypothetical protein F53H8.2 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000
 C;Accession: T34297
 R;Bradshaw, H.; Gattung, S.
 A;Description: The sequence of *C. elegans* cosmid F53H8.
 A;Reference number: Z21501
 A;Accession: T34297
 A;Status: preliminary; translated from GB/EMBL/DDBJ

Query Match
 Best Local Similarity 44.1%; Score 869.5; DB 2; Length 410;
 Matches 167; Conservative 76; Mismatches 99; Indels 5; Gaps 4;

QY 6 KVFKKCAPNGKVTLQMGKRDFTDHFVSGVERIDGIVVLVLDDEYIRDNRKVFGQIVCSFRYGR 65
 Db 8 RVFKKSSSPNCKVTLQMGKRDFTDHFVSGVERIDGIVVLVLDDEYIRDNRKVFGQIVCSFRYGR 65
 QY 66 EDEEVMLNFGQKELCLASEQIVPRPEKSDEQTKLQERLKKGSNAIPFTENISPNAPS 125
 Db 67 EDLDVIGLSFRKDLIATYQAFPPMPNPPRPPTRQLD-RKVFTVLTCAFRYGR 66
 QY 126 SVTLQOGEDDNGDPGVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQOPCTL 186
 Db 127 SVTLQGPEDTGKACCGVDFEIRACAKSIEBKSHKRNSVRVLRVKQFAPEKPGQPSAE 186
 QY 186 VRKDFMLSPGELEEVTLKDQKLQYLHGERIGVNICIRNNSNKMKKKIKAMVQOGVWLFQ 245
 Db 187 TTRHFLMSDRSLHIEASLDKELLYHGEPLNVNVHVTNNSTKTVKIKVSYROVADICLFS 246
 QY 246 NGSYRNTVASLETSEGCP1QPGSSLQKVMVLTPLISSNKORRGIAQIKRQDQCLAS 304
 Db 247 TAQYKCPVVAQLEQDD-QVSPSSTCKYVITIPLISDNREKRLGALDGKLKHEDTNLAS 305
 QY 305 TLLAQPDQDARFGVILSYAVKVKLFLGAGGELSAELPFLVMPKPG---TKAKVIIHAD 361
 Db 362 SQADVET---FQDIDQQAQSVDFE 363
 Db 364 SDPPIDTLLIREFEMNSQDDDFVFE 389

RESULT 15
 A59279 hypothetical protein F53H8.2 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000
 C;Accession: T34297
 R;Bradshaw, H.; Gattung, S.
 A;Description: The sequence of *C. elegans* cosmid F53H8.
 A;Reference number: Z21501
 A;Accession: T34297
 A;Status: preliminary; translated from GB/EMBL/DDBJ

Query Match
 Best Local Similarity 44.1%; Score 869.5; DB 2; Length 410;
 Matches 167; Conservative 76; Mismatches 99; Indels 5; Gaps 4;

QY 6 KVFKKCAPNGKVTLQMGKRDFTDHFVSGVERIDGIVVLVLDDEYIRDNRKVFGQIVCSFRYGR 65
 Db 8 RVFKKSSSPNCKVTLQMGKRDFTDHFVSGVERIDGIVVLVLDDEYIRDNRKVFGQIVCSFRYGR 65
 QY 66 EDEEVMLNFGQKELCLASEQIVPRPEKSDEQTKLQERLKKGSNAIPFTENISPNAPS 125
 Db 67 EDLDVIGLSFRKDLIATYQAFPPMPNPPRPPTRQLD-RKVFTVLTCAFRYGR 66
 QY 126 SVTLQOGEDDNGDPGVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQOPCTL 186
 Db 127 SVTLQGPEDTGKACCGVDFEIRACAKSIEBKSHKRNSVRVLRVKQFAPEKPGQPSAE 186
 QY 186 VRKDFMLSPGELEEVTLKDQKLQYLHGERIGVNICIRNNSNKMKKKIKAMVQOGVWLFQ 245
 Db 187 TTRHFLMSDRSLHIEASLDKELLYHGEPLNVNVHVTNNSTKTVKIKVSYROVADICLFS 246
 QY 246 NGSYRNTVASLETSEGCP1QPGSSLQKVMVLTPLISSNKORRGIAQIKRQDQCLAS 304
 Db 247 TAQYKCPVVAQLEQDD-QVSPSSTCKYVITIPLISDNREKRLGALDGKLKHEDTNLAS 305
 QY 305 TLLAQPDQDARFGVILSYAVKVKLFLGAGGELSAELPFLVMPKPG---TKAKVIIHAD 361
 Db 362 SQADVET---FQDIDQQAQSVDFE 363
 Db 364 SDPPIDTLLIREFEMNSQDDDFVFE 389

RESULT 15
 A59279 hypothetical protein F53H8.2 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000
 C;Accession: T34297
 R;Bradshaw, H.; Gattung, S.
 A;Description: The sequence of *C. elegans* cosmid F53H8.
 A;Reference number: Z21501
 A;Accession: T34297
 A;Status: preliminary; translated from GB/EMBL/DDBJ

Query Match
 Best Local Similarity 44.1%; Score 869.5; DB 2; Length 410;
 Matches 167; Conservative 76; Mismatches 99; Indels 5; Gaps 4;

QY 6 KVFKKCAPNGKVTLQMGKRDFTDHFVSGVERIDGIVVLVLDDEYIRDNRKVFGQIVCSFRYGR 65
 Db 8 RVFKKSSSPNCKVTLQMGKRDFTDHFVSGVERIDGIVVLVLDDEYIRDNRKVFGQIVCSFRYGR 65
 QY 66 EDEEVMLNFGQKELCLASEQIVPRPEKSDEQTKLQERLKKGSNAIPFTENISPNAPS 125
 Db 67 EDLDVIGLSFRKDLIATYQAFPPMPNPPRPPTRQLD-RKVFTVLTCAFRYGR 66
 QY 126 SVTLQOGEDDNGDPGVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQOPCTL 186
 Db 127 SVTLQGPEDTGKACCGVDFEIRACAKSIEBKSHKRNSVRVLRVKQFAPEKPGQPSAE 186
 QY 186 VRKDFMLSPGELEEVTLKDQKLQYLHGERIGVNICIRNNSNKMKKKIKAMVQOGVWLFQ 245
 Db 187 TTRHFLMSDRSLHIEASLDKELLYHGEPLNVNVHVTNNSTKTVKIKVSYROVADICLFS 246
 QY 246 NGSYRNTVASLETSEGCP1QPGSSLQKVMVLTPLISSNKORRGIAQIKRQDQCLAS 304
 Db 247 TAQYKCPVVAQLEQDD-QVSPSSTCKYVITIPLISDNREKRLGALDGKLKHEDTNLAS 305
 QY 305 TLLAQPDQDARFGVILSYAVKVKLFLGAGGELSAELPFLVMPKPG---TKAKVIIHAD 361
 Db 362 SQADVET---FQDIDQQAQSVDFE 363
 Db 364 SDPPIDTLLIREFEMNSQDDDFVFE 389

RESULT 15
 A59279 hypothetical protein F53H8.2 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000
 C;Accession: T34297
 R;Bradshaw, H.; Gattung, S.
 A;Description: The sequence of *C. elegans* cosmid F53H8.
 A;Reference number: Z21501
 A;Accession: T34297
 A;Status: preliminary; translated from GB/EMBL/DDBJ

Query Match
 Best Local Similarity 44.1%; Score 869.5; DB 2; Length 410;
 Matches 167; Conservative 76; Mismatches 99; Indels 5; Gaps 4;

QY 6 KVFKKCAPNGKVTLQMGKRDFTDHFVSGVERIDGIVVLVLDDEYIRDNRKVFGQIVCSFRYGR 65
 Db 8 RVFKKSSSPNCKVTLQMGKRDFTDHFVSGVERIDGIVVLVLDDEYIRDNRKVFGQIVCSFRYGR 65
 QY 66 EDEEVMLNFGQKELCLASEQIVPRPEKSDEQTKLQERLKKGSNAIPFTENISPNAPS 125
 Db 67 EDLDVIGLSFRKDLIATYQAFPPMPNPPRPPTRQLD-RKVFTVLTCAFRYGR 66
 QY 126 SVTLQOGEDDNGDPGVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQOPCTL 186
 Db 127 SVTLQGPEDTGKACCGVDFEIRACAKSIEBKSHKRNSVRVLRVKQFAPEKPGQPSAE 186
 QY 186 VRKDFMLSPGELEEVTLKDQKLQYLHGERIGVNICIRNNSNKMKKKIKAMVQOGVWLFQ 245
 Db 187 TTRHFLMSDRSLHIEASLDKELLYHGEPLNVNVHVTNNSTKTVKIKVSYROVADICLFS 246
 QY 246 NGSYRNTVASLETSEGCP1QPGSSLQKVMVLTPLISSNKORRGIAQIKRQDQCLAS 304
 Db 247 TAQYKCPVVAQLEQDD-QVSPSSTCKYVITIPLISDNREKRLGALDGKLKHEDTNLAS 305
 QY 305 TLLAQPDQDARFGVILSYAVKVKLFLGAGGELSAELPFLVMPKPG---TKAKVIIHAD 361
 Db 362 SQADVET---FQDIDQQAQSVDFE 363
 Db 364 SDPPIDTLLIREFEMNSQDDDFVFE 389

RESULT 15
 A59279 hypothetical protein F53H8.2 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000
 C;Accession: T34297
 R;Bradshaw, H.; Gattung, S.
 A;Description: The sequence of *C. elegans* cosmid F53H8.
 A;Reference number: Z21501
 A;Accession: T34297
 A;Status: preliminary; translated from GB/EMBL/DDBJ

Query Match
 Best Local Similarity 44.1%; Score 869.5; DB 2; Length 410;
 Matches 167; Conservative 76; Mismatches 99; Indels 5; Gaps 4;

QY 6 KVFKKCAPNGKVTLQMGKRDFTDHFVSGVERIDGIVVLVLDDEYIRDNRKVFGQIVCSFRYGR 65
 Db 8 RVFKKSSSPNCKVTLQMGKRDFTDHFVSGVERIDGIVVLVLDDEYIRDNRKVFGQIVCSFRYGR 65
 QY 66 EDEEVMLNFGQKELCLASEQIVPRPEKSDEQTKLQERLKKGSNAIPFTENISPNAPS 125
 Db 67 EDLDVIGLSFRKDLIATYQAFPPMPNPPRPPTRQLD-RKVFTVLTCAFRYGR 66
 QY 126 SVTLQOGEDDNGDPGVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQOPCTL 186
 Db 127 SVTLQGPEDTGKACCGVDFEIRACAKSIEBKSHKRNSVRVLRVKQFAPEKPGQPSAE 186
 QY 186 VRKDFMLSPGELEEVTLKDQKLQYLHGERIGVNICIRNNSNKMKKKIKAMVQOGVWLFQ 245
 Db 187 TTRHFLMSDRSLHIEASLDKELLYHGEPLNVNVHVTNNSTKTVKIKVSYROVADICLFS 246
 QY 246 NGSYRNTVASLETSEGCP1QPGSSLQKVMVLTPLISSNKORRGIAQIKRQDQCLAS 304
 Db 247 TAQYKCPVVAQLEQDD-QVSPSSTCKYVITIPLISDNREKRLGALDGKLKHEDTNLAS 305
 QY 305 TLLAQPDQDARFGVILSYAVKVKLFLGAGGELSAELPFLVMPKPG---TKAKVIIHAD 361
 Db 362 SQADVET---FQDIDQQAQSVDFE 363
 Db 364 SDPPIDTLLIREFEMNSQDDDFVFE 389

RESULT 15
 A59279 hypothetical protein F53H8.2 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000
 C;Accession: T34297
 R;Bradshaw, H.; Gattung, S.
 A;Description: The sequence of *C. elegans* cosmid F53H8.
 A;Reference number: Z21501
 A;Accession: T34297
 A;Status: preliminary; translated from GB/EMBL/DDBJ

Query Match
 Best Local Similarity 44.1%; Score 869.5; DB 2; Length 410;
 Matches 167; Conservative 76; Mismatches 99; Indels 5; Gaps 4;

QY 6 KVFKKCAPNGKVTLQMGKRDFTDHFVSGVERIDGIVVLVLDDEYIRDNRKVFGQIVCSFRYGR 65
 Db 8 RVFKKSSSPNCKVTLQMGKRDFTDHFVSGVERIDGIVVLVLDDEYIRDNRKVFGQIVCSFRYGR 65
 QY 66 EDEEVMLNFGQKELCLASEQIVPRPEKSDEQTKLQERLKKGSNAIPFTENISPNAPS 125
 Db 67 EDLDVIGLSFRKDLIATYQAFPPMPNPPRPPTRQLD-RKVFTVLTCAFRYGR 66
 QY 126 SVTLQOGEDDNGDPGVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQOPCTL 186
 Db 127 SVTLQGPEDTGKACCGVDFEIRACAKSIEBKSHKRNSVRVLRVKQFAPEKPGQPSAE 186
 QY 186 VRKDFMLSPGELEEVTLKDQKLQYLHGERIGVNICIRNNSNKMKKKIKAMVQOGVWLFQ 245
 Db 187 TTRHFLMSDRSLHIEASLDKELLYHGEPLNVNVHVTNNSTKTVKIKVSYROVADICLFS 246
 QY 246 NGSYRNTVASLETSEGCP1QPGSSLQKVMVLTPLISSNKORRGIAQIKRQDQCLAS 304
 Db 247 TAQYKCPVVAQLEQDD-QVSPSSTCKYVITIPLISDNREKRLGALDGKLKHEDTNLAS 305
 QY 305 TLLAQPDQDARFGVILSYAVKVKLFLGAGGELSAELPFLVMPKPG---TKAKVIIHAD 361
 Db 362 SQADVET---FQDIDQQAQSVDFE 363
 Db 364 SDPPIDTLLIREFEMNSQDDDFVFE 389

RESULT 15
 A59279 hypothetical protein F53H8.2 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000
 C;Accession: T34297
 R;Bradshaw, H.; Gattung, S.
 A;Description: The sequence of *C. elegans* cosmid F53H8.
 A;Reference number: Z21501
 A;Accession: T34297
 A;Status: preliminary; translated from GB/EMBL/DDBJ

Query Match
 Best Local Similarity 44.1%; Score 869.5; DB 2; Length 410;
 Matches 167; Conservative 76; Mismatches 99; Indels 5; Gaps 4;

QY 6 KVFKKCAPNGKVTLQMGKRDFTDHFVSGVERIDGIVVLVLDDEYIRDNRKVFGQIVCSFRYGR 65
 Db 8 RV

A;Residues: 1-454 <BRA>
A;Cross-references: EMBL:U41023; PIDN:AAA82342.1; CESP:F53H8.2
C;Genetics:
A;Gene: CESP:F53H8.2
A;Introns: 11/2; 61/1; 155/3; 189/2; 237/3; 290/2; 338/2; 389/3; 416/2
C;Superfamily: arrestin

Search completed: February 9, 2005, 23:46:47
Job time : 43 secs

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Copyright (c) 1993 - 2005 Compugen Ltd.	GenCore version 5.1.6				
OM protein - protein search, using sw model					
Run on:	February 9, 2005, 23:23:51 ; Search time 64 seconds (without alignments) 3064.474 Million cell updates/sec				
Title:	US-10-056-405-2				
Perfect score:	1973				
Sequence:	1 MVYNFKVKKCAPNGKVLY.....ADVETFRQDTIDQQASVDFE 383				
Scoring table:	BLOSUM62				
Searched:	Gapop 10.0 , Gapext 0.5				
Total number of hits satisfying chosen parameters:	1612378				
Minimum DB seq length:	0				
Maximum DB seq length:	2000000000				
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries				
Database :	UniProt_03:*				
	1: uniprot_sprot:*				
	2: uniprot_trembl:*				
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					
SUMMARIES					
Result No.	Score	Query Match	Length	DB ID	Description
1	1973	100.0	383	2 Q95NF3	Q95nf3 anopheles g
2	1973	100.0	417	2 Q7PMGS	Q7pmgs anopheles g
3	1515	76.8	381	2 Q9BIG9	Q9big9 ascalaphus
4	1499	76.0	381	1 ARRH_HELVI	P55274 heliothis v
5	1384	70.1	364	1 ARRA_DROME	P15372 drosophila
6	1335	67.7	363	1 ARRI_CALVI	P51486 calliphora
7	1254	63.6	245	2 Q6VPP0	Q6vppo anopheles g
8	1036	52.5	431	2 QTQ2V9	Q7q2v9 anopheles g
9	1023	51.8	398	2 Q66GU6	Q66gu6 anopheles g
10	1023	51.8	401	2 Q7Q5Q8	Q7q5q8 anopheles g
11	1002	50.8	470	2 Q9V393	Q9v393 drosophila
12	993.5	50.4	407	1 ARRH_LOCM1	P32122 locusta mig
13	982.5	49.8	401	1 ARR_B_DROME	P19107 drosophila
14	977.5	49.5	401	1 ARR_B_DROME	P19108 drosophila
15	937.5	47.5	400	1 ARRB_CALVI	P51487 calliphora
16	931	47.2	400	1 ARRH_LIMPO	P51484 limulus pol
17	931	47.2	419	2 Q86BW6	Q86bw6 halocynthia
18	922.5	46.8	418	2 Q8MYB1	Q8myb1 ciona intes
19	919	46.6	412	2 Q641DB	Q641db xenopus lae
20	912.5	46.2	410	2 Q8BTJ5	Q8btj5 mus musculus
21	904.5	45.8	418	2 Q8BWGB	Q8bwgb mus musculus
22	903.5	45.8	418	1 ARR1_BOVIN	P17870 bos taurus
23	903.5	45.8	418	1 ARR1_RAT	P29066 rattus norvegicus
24	900.5	45.6	418	1 ARR1_HUMAN	P49407 homo sapiens
25	893	45.3	408	2 Q7T2D2	Q7t2d2 brachydanio
26	888.5	45.0	435	1 ARRB_CAEEL	P51485 caenorhabditis
27	887	45.0	420	1 ARR2_BOVIN	P32120 bos taurus
28	885	44.9	409	1 ARR2_HUMAN	P32121 homo sapiens
29	881	44.7	409	2 Q6ICT3	Q6ict3 homo sapiens
30	880.5	44.6	410	1 ARR1_RABIT	Q95223 orctolagrus
31	880	44.6	408	2 Q6DFC4	Q6dfc4 xenopus lae

ALIGNMENTS

RESULT 1	ID Q95NF3	PRELIMINARY;	PRT;	383 AA.
	AC Q95NF3;	DT 01-DEC-2001 (TREMBLrel. 19, Created)		
	DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)	DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)		
	DE Arrestin.			
	GN Anopheles_gambiae (African malaria mosquito).			
	OS Eukaryota; Metazoa; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.			
	OC NCBI_TaxID=7165;			
	RN [1]			
	SEQUENCE FROM N.A.			
	RC TISSUE=Antennae, and Head;			
	RX MEDLINE=21680430; PubMed=11822731;			
	RA Ricci_I, Santolamazza_F, Costantini_C, Favia_G;			
	RT "Molecular characterization and chromosomal mapping of transcripts having tissue-specific expression in the malaria mosquito anopheles gambiae: possible involvement in visual or olfactory processes.";			
	RT parastol. Res. 88:1-8 (2002).			
	RL [2]			
	RN SEQUENCE FROM N.A.			
	RC STRAIN=G3;			
	RX MEDLINE=21819361; PubMed=11792843; DOI=10.1073/pnas.022505499;			
	RA Merrill_C.E., Riesgo-Escovar_J., Pitts_R.J., Kafatos_F.C., Carlson_J.R., Zwiebel_L.J.;			
	RT "Visual arrestins in olfactory pathways of Drosophila and the malaria vector mosquito Anopheles gambiae.";			
	RT Proc. Natl. Acad. Sci. U.S.A. 99:1633-1638 (2002).			
	RL EMBL; AJ304409; CAC39103.2; -.			
	DR EMBL; AY017417; AAG54081.1; -.			
	DR HSSP; P17870; 1G4M.			
	DR GO; GO:0007600; P:sensory perception; IEA.			
	DR GO; GO:0007165; P:signal transduction; IEA.			
	DR InterPro; IPR00698; Arrestin.			
	DR InterPro; IPR01022; Arrestin_C.			
	DR InterPro; IPR01021; Arrestin_N.			
	DR Pfam; PF02752; Arrestin_C; 1.			
	DR Pfam; PF00339; Arrestin_N; 1.			
	DR PRINTS; PR00309; ARRESTIN.			
	DR PROSITE; PS0295; ARRESTINS; 1.			
	DR SEQUENCE; PS0295; ARRESTINS; 1.			
	QY Query Match 100.0%; Score 1973; DB 2; Length 383;			
	Best Local Similarity 100.0%; Pred. No. 1.1e-144;			
	Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
	QY 1 MVYNFKVKKCAPNGKVLYMGRDFVDRYSGVLEPIDGIVVLDDEYIRDNRKVFQIVCS 60			
	Db 1 MVYNFKVKKCAPNGKVLYMGRDFVDRYSGVLEPIDGIVVLDDEYIRDNRKVFQIVCS 60			
	QY 61 FRYGREEDEVMLGLNFOKECLCLASEQIYPRPEKSDEQTKLQERLLKKLGNSNAIPPTFNS 120			

Db 61 FRYGREDDEVMLNFOKEICLASEQIYPRPEKSDEQTKLQERLKKLGNSNAPFTNIS 120
 QY 1.21 PNAPSSVTLQGEDDNGDPGCVYYVKIFAGESETDRTHRSTVTGIRKIQFAPTKQGQ 180
 Db 1.21 PNAPSSVTLQGEDDNGDPGCVYYVKIFAGESETDRTHRSTVTGIRKIQFAPTKQGQ 180
 QY 181 QPCTLVRKDFMLSPGELELEVTLQDQLYLHGERIGVNICIRNNSNKMKKIKAMVQGVD 180
 Db 1.81 QPCTLVRKDFMLSPGELELEVTLQDQLYLHGERIGVNICIRNNSNKMKKIKAMVQGVD 180
 QY 241 VLFQONGSYRNTVASLETSEGCPIQGSSLQKVMYLTPLLSSNKKRGTALDGQIKRQDQ 240
 Db 241 VLFQONGSYRNTVASLETSEGCPIQGSSLQKVMYLTPLLSSNKKRGTALDGQIKRQDQ 240
 QY 3.01 CLASTLLAQPDQDQDAFGVIIISYAVKVLFLGALGELSAELPFLVMHPKPGTKAKVHA 360
 Db 3.01 CLASTLLAQPDQDQDAFGVIIISYAVKVLFLGALGELSAELPFLVMHPKPGTKAKVHA 360
 QY 361 DSQADVETFRQDTIDQQASVDFE 383
 Db 361 DSQADVETFRQDTIDQQASVDFE 383
 361 DSQADVETFRQDTIDQQASVDFE 383
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 361 DSQADVETFRQDTIDQQASVDFE 383
 395 DSQADVETFRQDTIDQQASVDFE 417

RESULT 2

Q7PMG5
 ID Q7PMG5
 AC Q7PMG5;
 DT 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DE ENSANGP0000012569 (Fragment).
 OS Name=ENSANGG0000010080;
 OC Anopheles_gambiae str. PEST.
 OC Neoptera; Arthropoda; Hexapoda; Insecta; Pterygota;
 OX NCBI_TaxID=180454;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PEST;
 RA Anopheles Genome Sequencing Consortium;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 EMBL; AAAH01008980; EAA13874.2; -.
 DR HSSP; P17870; 1G4M.
 DR GO; GO:000760; P:sensory perception.
 DR GO; GO:0007165; P:signal transduction; IBA.
 DR InterPro; IPR00698; Arrestin.
 DR InterPro; IPR011022; Arrestin_C.
 DR Pfam; PF02752; Arrestin_C; 1.
 DR PRINTS; PR00339; Arrestin_N; 1.
 DR PROSITE; PS002099; Arrestin.
 DR PROSITE; PS00295; Arrestin; 2.
 DR PROSITE; PS00295; Arrestins; 1.
 SQ SEQUENCE 417 AA; 46591 MW; 4EE98A3C32257FC0 CRC64;
 Query Match Best Local Similarity 100.0%; Score 1973; DB 2; Length 417;
 Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MVYNFKVKKKCAPNGKVTLYMGRDFDHSVGVPERIDGIVVLDDEVYIRDNRKVFGQIVCS 60
 Db 35 MVYNFKVKKKCAPNGKVTLYMGRDFDHSVGVPERIDGIVVLDDEVYIRDNRKVFGQIVCS 60
 QY 61 FRYGREDDEVMLNFOKEICLASEQIYPRPEKSDEQTKLQERLKKLGNSNAPFTNIS 120
 Db 95 FRYGREDDEVMLNFOKEICLASEQIYPRPEKSDEQTKLQERLKKLGNSNAPFTNIS 120
 1.21 PNAPSSVTLQGEDDNGDPGCVYYVKIFAGESETDRTHRSTVTGIRKIQFAPTKQGQ 180
 QY 180 QPCTLVRKDFMLSPGELELEVTLQDQLYLHGERIGVNICIRNNSNKMKKIKAMVQGVD 180
 Db 155 PNAPSSVTLQGEDDNGDPGCVYYVKIFAGESETDRTHRSTVTGIRKIQFAPTKQGQ 214
 QY 181 QPCTLVRKDFMLSPGELELEVTLQDQLYLHGERIGVNICIRNNSNKMKKIKAMVQGVD 214
 Db 215 QPCTLVRKDFMLSPGELELEVTLQDQLYLHGERIGVNICIRNNSNKMKKIKAMVQGVD 240
 QY 241 VLFQONGSYRNTVASLETSEGCPIQGSSLQKVMYLTPLLSSNKKRGTALDGQIKRQDQ 240
 Db 241 VLFQONGSYRNTVASLETSEGCPIQGSSLQKVMYLTPLLSSNKKRGTALDGQIKRQDQ 274
 QY 275 VLFQONGSYRNTVASLETSEGCPIQGSSLQKVMYLTPLLSSNKKRGTALDGQIKRQDQ 300
 Db 301 CLASTLLAQPDQDQDAFGVIIISYAVKVLFLGALGELSAELPFLVMHPKPGTKAKVHA 360
 QY 335 CLASTLLAQPDQDQDAFGVIIISYAVKVLFLGALGELSAELPFLVMHPKPGTKAKVHA 360
 Db 361 DSQADVETFRQDTIDQQASVDFE 383
 QY 361 DSQADVETFRQDTIDQQASVDFE 383
 Db 395 DSQADVETFRQDTIDQQASVDFE 417

RESULT 3

Q9BIG9
 ID Q9BIG9
 AC Q9BIG9;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DE Arrestin. Name=arrl;
 OS Ascalaphus macaronius.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OX NCBI_TaxID=146496;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Head;
 RX MEDLINE=21184354; PubMed=11287006; DOI=10.1016/S0014-5793(01)02287-6;
 RA Bentrop J.; Schillo M.; Gerdon G.; Draslar G.; Paulsen R.;
 RT "UV-light-dependent binding of a visual arrestin 1 isoform to
 RL photoreceptor membranes in a neuropteran (Ascalaphus) compound eye."
 DR EMBL; AJ303080; CAC36938.1; -.
 DR HSSP; P17870; 1G4M.
 DR GO; GO:000760; P:sensory perception.
 DR GO; GO:0007165; P:signal transduction; IBA.
 DR InterPro; IPR00698; Arrestin.
 DR InterPro; IPR011022; Arrestin_C.
 DR Pfam; PF02752; Arrestin_C; 1.
 DR PRINTS; PR00339; Arrestin_N; 1.
 DR PROSITE; PR00309; Arrestin_N; 1.
 DR PROSITE; PS00295; Arrestin.
 DR PROSITE; PS00295; Arrestins; 1.
 SQ SEQUENCE 381 AA; 42789 MW; 451DEF465969857D CRC64;
 Query Match Best Local Similarity 76.8%; Score 1515; DB 2; Length 381;
 Matches 289; Conservative 75.7%; Pred: No. 3.7e-109; Length 381;
 QY 1 MVYNFKVKKKCAPNGKVTLYMGRDFDHSVGVPERIDGIVVLDDEVYIRDNRKVFGQIVCS 59
 Db 1 MVYNFKVKKKCAPNGKVTLYMGRDFDHSVGVPERIDGIVVLDDEVYIRDNRKVFGQIVCS 60
 QY 60 SFRYGREDEVMLNFOKEICLASEQIYPRPEKSDEQTKLQERLKKLGNSNAPFTNIS 119
 Db 61 SFRYGREDEVMLNFOKEICLASEQIYPRPEKSDEQTKLQERLKKLGNSNAPFTNIS 120
 QY 120 SPNAPSSVTLQGEDDNGDPGCVYYVKIFAGESETDRTHRSTVTGIRKIQFAPTKQGQ 119
 Db 119 PPNAPATITLQPGAEEDQGEPGCVQYFLKAFVGESETDRPHARSSVSMQIRKIQYAPSKQG 179
 QY 180 QPCTLVRKDFMLSPGELELEVTLQDQLYLHGERIGVNICIRNNSNKMKKIKAMVQGVD 178
 Db 179 RQPCVVRKDFMLSPGDLLELEVTLQDQLYLHGERIGVNICIRNNSNKMKKIKAMVQGVD 239
 QY 180 QPCTLVRKDFMLSPGELELEVTLQDQLYLHGERIGVNICIRNNSNKMKKIKAMVQGVD 238

Qy 240 DVVLFONGSYRNTVASLETSGCPIOPGSSLOKVMYLTPLLSSNKQRGTAIDGQIKRQD 299
 Db 239 DVVLFONGQYRTTIALETOEGCPIQPSALQKVMYLPSNKRQGIAIDGQIKRQD 298
 Qy 300 OCLASTTLAOPDORDAFGVVILSYAVVKVLFLGALGGELSAELPFVLMAPKPGTKAKVH 359
 Db 299 TNLASTTLLAOPDQDAFGIIVSYAVVKVLFLGALGGELAELPFLMHPRP-ERNKFIH 357
 Qy 360 ADSQADVETFRQDTIDQQASVD 381
 Db 358 ADSQADVEMFRQDTVD--PSVD 377

RESULT 4

ARRH_HELVI STANDARD; PRT; 381 AA.

ID _ARRH_HELVI STANDARD; PRT; 381 AA.

AC P55274; P15372; Q9VJA8; P15372; Q9VJA8;

DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Arrestin homolog.

OS *Heliothis virescens* (Noctuid moth) (Owl moth).
 Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea; NCBI_TaxID=7102;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Antenna;
 RX MEDLINE=93199955; PubMed=8452755; DOI=10.1016/0898-6568(93)90009-B;

RA Raming K., Freitag J., Krieger J., Breer H.;

RT "Arrestin-subtypes in insect antennae.";
 Cell. Signal. 5:69-80(1993).

CC -1 SIMILARITY: Belongs to the arrestin family.

DR PIR; B56607; B56607.

DR HSSP; P17870; IG4M.

DR InterPro; IPR000698; Arrestin.

DR InterPro; IPR011022; Arrestin_C.

DR InterPro; IPR011021; Arrestin_N.

DR Pfam; PF02752; Arrestin_C; 1.

DR Ptam; PF00339; Arrestin_N; 1.

DR PRINTS; PR00309; ARRESTIN.

DR ProDom; PD002099; Arrestin; 2.

DR PROSITE; PS00295; ARRESTINS; 1.

KW Sensory transduction.

SQ SEQUENCE 381 AA; 42747 MW; 84BB92B1B3DA573 CRC64;

Query Match Best Local Similarity 76.0%; Score 1499; DB 1; Length 381; Matches 277; Conservative 51; Mismatches 51; Indels 2; Gaps 2;

Best Local Similarity 72.7%; Pred. No. 6.5e-108; Score 1499; DB 1; Length 381; Matches 277; Conservative 51; Mismatches 51; Indels 2; Gaps 2;

Matches 277; Conservative 51; Mismatches 51; Indels 2; Gaps 2;

Query 1 MVYNFKVFKKCAPNGKVRDFVHDVSGVVERPDKDPEYIRDNRKVFGQIVCS 60
 Db 1 MVYNFKVFKKCAPNGKVRDFVHDVSGVVERPDKDPEYIRDNRKVFGQIVCS 60

Query 61 FRYGREEDEVMGLNPKELCLASSEQTYPRPEKSDKEQTQKLERLLKKUGSNALPFTFNIS 120
 Db 60 FRYGREEDEVMGLNPKELCLASSEQTYPRPEKSDKEQTQKLERLLKKUGSNALPFTFNIS 120

Query 121 PNAPSSVTQLOQGEDDNGDPGCVSYVKFAGESETDRTHRSTVTLGIRKIQFAPTKQGQ 180
 Db 120 PGAPGSVILQPGLEDDGEPCGVQYVKIFVGDSSEIDRSHRSTVALGIRKVOYAPAKPCC 179

Query 181 QPCTLVRKDFMLSPGELELEVTLDKQLYLHGERIGNICIRNNSNKMKKKIKAMVQGVD 240
 Db 180 QPCTLVRKDFVLSPGQOLEBLTLDKQLYIGETAVNMCVRNHSNKKVKKIACIQQGVD 239

Query 241 VVLFONGSYRNTVASLETSGCPIOPGSSLOKVMYLTPLLSSNKQRGIAIDGQIKRQD 300
 Db 240 VVLFONGQYRNVNIVASIEQDGCPLQPGSSLQKVVLHPTLAHNDRKGIALDGQQLRSR 299

Query 301 CLASTTLLAOPDQDAFGIIVSYAVVKVLFLGALGGELSAELPFVLMAPKPGTKAKVH 360

RESULT 5

ARRA_DROME STANDARD; PRT; 364 AA.

ID _ARRA_DROME STANDARD; PRT; 364 AA.

AC P15372; Q9VJA8; P15372; Q9VJA8;

DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)

DE Phosrestin_I1 (Arrestin A) (Arrestin 1).

GN Name=Arr1; Synonyms=ArrA; ORFNames=CG5711;

OS Drosophila melanogaster (Fruit fly).
 Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.

RX MEDLINE=90138925; PubMed=1689056;

RA Hyde D.R., Mecklenburg K.L., Pollock J.A., Vihtelic T.S., Benzer S.;

RT "Twenty Drosophila visual system cDNA clones: one is a homolog of human arrestin.";
 Proc. Natl. Acad. Sci. U.S.A. 87:1003-1007(1990).

RN [2]

SEQUENCE FROM N.A.

RC STRAIN=Berkeley;

RX MEDLINE=90138926; PubMed=2105491;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahleke C., Davenport L.B., Davies P., de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin R.K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann R., Fosler C., Gabriel A.E., Garg N.S., Gelbart W.M., Glaser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitt A.A., Li J.H., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milashina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacble J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shieh B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of *Drosophila melanogaster*,"
 RT Science 287:2185-2195 (2000).
 RL [4] GENOME REANNOTATION.
 RN MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield D.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.; "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review"; Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002).
 RN [15] SEQUENCE FROM N.A.
 RC STRAIN=Berkeley; TISSUE=Head;
 RX MEDLINE=22426066; PubMed=12537569;
 RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
 RA George R.A., Carlson H., Krommiller B., Paclob J.M., Park S., Wan K.H.,
 RA Rubin G.M., Celniker S.E., "A *Drosophila* full-length cDNA resource,"
 RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8 (2002).
 RN [16] PHOSPHORYLATION.
 RP MEDLINE=91282780; PubMed=1905538;
 RA Matsumoto H., Yamada T.,
 RT "Phosrestins I and II: arrestin homologs which undergo differential
 RL light-induced phosphorylation in the *Drosophila* photoreceptor in
 Biomed. Biophys. Res. Commun. 177:1306-1312 (1991).
 RN [17] FUNCTION.
 RX MEDLINE=93303590; PubMed=8316831;
 RA Dolph P.J., Ranganathan R., Colley N.J., Hardy R.W., Socolich M.,
 RT Zuker C.S.; "Arrestin function in inactivation of G protein-coupled receptor
 RL rhodopsin in vivo"; Science 260:1910-1916 (1993).
 CC -I- FUNCTION: Regulates photoreceptor cell deactivation.
 CC proteins are mediators of rhodopsin inactivation and are essential
 CC for the termination of the phototransduction cascade.
 CC -I- TISSUE SPECIFICITY: Expressed specifically and abundantly in the
 CC photoreceptors. Inner and outer segments, and the inner plexiform
 CC regions of the retina.
 CC -I- PTM: Phosphorylated, but does not undergo light-induced
 CC phosphorylation.
 CC -I- SIMILARITY: Belongs to the arrestin family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC modified and this statement is not removed. Usage by and for commercial
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 CC or send an email to license@isb-sib.ch).
 DR EMBL; M30177; -; NOT_ANNOTATED_CDS.
 DR EMBL; M30140; AAA28380.1; -.
 DR EMBL; AE003657; AAF53644.1; -.
 DR PIR; A34867; AAL27635.1; -.
 DR HSSP; P1870; 1G4M.
 DR IntAct; P15372; -.
 DR FlyBase; FBgn000120; Arrl.
 DR GO; GO:0005624; C:membrane fraction; IDA.
 DR GO; GO:0016028; C:rhabdomere; IDA.
 DR GO; GO:0016060; P:metarhabdomere; IDA.
 DR InterPro; IPR000698; Arrestin.
 DR InterPro; IPR011022; Arrestin_C.

RESULT 6

ARR1_CALVI	ID	ARR1_CALVI	STANDARD	PRR	363 AA.
DT	01-OCT-1996	(Rel. 34, Created)			
DT	05-JUL-2004	(Rel. 44, Last sequence update)			
DE		Phosrestin II (Arrestin A) (Arrestin 1).			
GN		Name=ARR1			
OS		Calliphora vicina (Blue blowfly) (Calliphora erythrocephala).			
OC		Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Oestroidea;			
OC		Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;			
OC		Calliphoridae; Calliphora; NCBI_TaxID=7373;			
OX					
RN	[1]				
RP		SEQUENCE FROM N.A.			
RC		TISSUE=Retina;			
RA		MEDLINE=95014564; PubMed=7929436;			
RT		"Mechanism of arrestin 2 function in rhabdomeric photoreceptors.";			
RL		J. Biol. Chem. 269:26969-26975 (1994).			
CC		-I- SIMILARITY: Belongs to the arrestin family.			
CC		This SWISS-PROT entry is copyright. It is produced through a collaboration CC between the European Bioinformatics Institute and the EMBL outstation - CC use by non-profit institutions as long as its content is in no way CC modified and this statement is not removed. Usage by and for commercial CC entities requires a license agreement (see http://www.isb-sib.ch/announce/). CC or send an email to license@isb-sib.ch).			

DR EMBL; X79072; CAA55672.1; -.

DR PIR; A55081; A55081.

DR HSSP; P17870; 1G4M.

DR InterPro; IPR00698; Arrestin.

DR InterPro; IPR011022; Arrestin_C.

DR InterPro; IPR011021; Arrestin_N.

DR InterPro; IPR011021; Arrestin_C.

DR Pfam; PF02752; Arrestin_C; 1.

DR Pfam; PF00339; Arrestin_N; 1.

DR Prints; PR00309; ARRESTIN.

DR ProDom; PD002099; Arrestin; 2.

DR ProDom; PD002099; Arrestin; 2.

DR PROSITE; PS00295; ARRESTINS; 1.

KW Sensory transduction; vision.

SQ SEQUENCE 363 AA; 40680 MW; 7C345DB18E46C23E CRC64;

Query Match 67.7%; Score 1335; DB 1; Length 363; Best Local Similarity 67.4%; Pred. No. 3.2e-95; Matches 248; Conservative 57; Mismatches 55; Indels 8; Gaps 2;

Qy 1 MVVNFKVKKCAPNGKVTLNGKRDENVHSGVEPIDGIVVLDEYIRDNRKVFGQIVCS 60

Db 1 MVVNFKVKKASPNNMVTLYMNRREFVDSVTQEVPGDGVVVLDEYIRQNRKIFVQOLCN 60

Qy 61 FRYGREDDEEVMLNFOKEBLCLASBQIYPRPEKSDEQTKLQERLLKKLGSNAIPFTENIS 120

Db 61 FRYGREDDEMIGLRFQKELVLIVSQPVYIPE-QKIDQLTRMQERLKKLGSNAIPFTENIS 120

Qy 121 PNAPPSSVTLOQGEDDNGDPCCGVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQ 180

Db 120 PSSPASVVLQKANDSTQPGVQYFVKVFAGENDCDRSHRSTVNLGIRKVQYAPTKTGI 179

Qy 181 QPCTLVRKDFMLSPGELELEVTLDKQLYLHGERIGVNICIRNNSNKMKVKKIKAMVQOGVD 240

Db 180 QPCTVVRKDFLISPGELELEVTLDRQLYHGEKISINICVRNNSNKVKKKIKAMVQOGID 239

Qy 241 VVLFQNGSYRNTVASLETSBGCPIQPGSSLQKVMYLTPLLSSNKORRGIALDQIKRQDQ 300

Db 240 WLFLQNGQFRNTIAFAESSEGCPLNPGSSLQKIMVLYVPLAANDRAGIAVEGDVVKHJKT 299

Qy 301 CLASTTLLAQPDORDAFGVVISYAVKVLFGLALGELSAELPFVLMHPKPGTKAKVHADSDQAVET 360

Db 300 SLASTTLLAQEARDAGFLIVSYAVKVLFGLALGELCAELPFILMHPKPSLKA---- 354

Qy 361 DSQADVENT 368

Db 355 - -QPEAET 360

RESULT 7

Q6VPP0 PRELIMINARY; PRT; 245 AA.

ID Q6VPP0; PRELIMINARY; PRT; 245 AA.

AC Q6VPP0; PRELIMINARY; PRT; 245 AA.

DT 05-JUL-2004 (TREMBLrel. 27, Created)

DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)

DE Arrestin (Fragment)

OS Anopheles gambiae (African malaria mosquito).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.

OX NCBI_TaxID=7155;

[1] SEQUENCE FROM N.A.

RP STRAIN=4ARR, Yaounde, and L3-5;

RA Morlais I., Poncon N., Simard F., Cohuet A., Fontenille D., Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY333991; AAR01116.1; -.

DR EMBL; AY333992; AAR01117.1; -.

DR EMBL; AY333993; AAR01118.1; -.

DR EMBL; AY333995; AAR01120.1; -.

DR EMBL; AY333996; AAR01121.1; -.

DR EMBL; AY333994; AAR01119.1; -.

DR HSSP; P08168; IAYR.

GO; GO:0007165; P:signal transduction; IEA.

DR InterPro; IPR00698; Arrestin.

DR InterPro; IPR011022; Arrestin_C.

DR InterPro; IPR011021; Arrestin_N.

DR InterPro; IPR011021; Arrestin_C; 1.

DR InterPro; IPR011021; Arrestin_N; 1.

DR Prints; PR00309; ARRESTIN.

DR ProDom; PD002099; Arrestin; 2.

DR FT NON-TER 1 1

FT NON-TER 245 245

SQ SEQUENCE 245 AA; 27038 MW; 86DBFF4520115DASP CRC64;

Query Match 63.6%; Score 1254; DB 2; Length 245; Best Local Similarity 100.0%; Pred. No. 3.7e-89; Matches 0; Mismatches 0; Indels 0; Gaps 0;

Db 129 LQGEDDNGDPCCGVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQOPCTLVK 188

Qy 189 DFMLSPGELELEVTLDKQLYLHGERIGVNICIRNNSNKMKVKKIKAMVQOGVDWLFONGS 248

Db 61 DFMLSPGELELEVTLDKQLYLHGERIGVNICIRNNSNKMKVKKIKAMVQOGVDWLFONGS 120

Qy 249 VRNTVASLETSEGCPIQPGSSLQKVMYLTPLLSSNKORRGIALDQIKRQDQCLASTTIL 308

Db 121 VRNTVASLETSEGCPIQPGSSLQKVMYLTPLLSSNKORRGIALDQIKRQDQCLASTTIL 180

Qy 309 AQPPQDRAFTGVVISYAVKVLFGLALGELSAELPFVLMHPKPGTKAKVHADSDQAVET 368

Db 181 AQPPQDRAFTGVVISYAVKVLFGLALGELCAELPFILMHPKPSLKA---- 240

Qy 369 FROQT 373

Db 241 FROQT 245

RESULT 8

Q7Q2V9 PRELIMINARY; PRT; 431 AA.

ID Q7Q2V9 PRELIMINARY; PRT; 431 AA.

AC Q7Q2V9; PRELIMINARY; PRT; 431 AA.

DT 01-MAR-2004 (TREMBLrel. 26, Created)

DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)

DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)

DE EbiP989 (Kurtz arrestin-like protein ARR) (Fragment); Name=ebiP989; Synonyms=ARRK; ORFNames=ENSANGG00000003863; OS Anopheles gambiae ssp. PEST.

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.

OX NCBITaxID=180454;

RN [1] SEQUENCE FROM N.A.

RP STRAIN=PEST;

RC Anopheles Genome Sequencing Consortium;

RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

RL NCBITaxID=180454;

RN [2] SEQUENCE FROM N.A.

RP STRAIN=PEST;

RC MEDLINE=23159591; PubMed=14986925;

RA Merrill C.E., Pitts R.J., Zwiebel L.J.;

RT "Molecular characterization of arrestin family members in the malaria vector mosquito, Anopheles gambiae.";

RL Insect Mol. Biol. 12:641-650 (2003).

CC -1 CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.

CC EMBL; AAB01008966; EAA13078.1; -.

DR EMBL; BK000997; DAA00889.1; -.

DR HSSP; P17870; 1G4M.

DR GO; GO:0007600; P:sensory perception; IEA.

DR GO; GO:0007165; P:signal transduction; IEA.

DR InterPro; IPR00698; Arrestin.

DR InterPro; IPR011022; Arrestin_C.

		Matches	204; Conservative	65; Mismatches	111; Indels	10; Gaps	7;
DR	InterPro; IPR011021; Arrestin_N.	Qy	1 MWYNFKVKCACPNGKVTLYMGKRDFFDHDVSGVEPIDGIVVLDDEYIRDNRKVFGQIVCS	60			
DR	Pfam; PF02752; Arrestin_C; 1.	Db	1 MWVAVKVKFVKCAPNGKVTLYMGKRDFFDHDVSGVEPIDGIVVLDDEYIRDNRKVFGQIVCS	60			
DR	PRINTS; PR00339; Arrestin_N; 1.	Qy	61 FRYGREREDEVMLNGLNFOKEIICLASEQIYPRPEKSDKQTKLQERLILKLGNSAIPFTFNIS	120			
DR	ProDom; PD002099; Arrestin.	Db	60 YRYGREGEDDEVMGVKFSKEMVLTKEQIKPM-ENAMNEMTPMQERLVRKLGANAFPTFHFP	118			
FT	PROSITE; PS00295; ARRESTINS; 1.	Qy	121 PNAQSSVTLQOQGEDDNGDPCCGSYVYVLFAGESETDRTHRSTVTLGIRKIOAFTKQGQ	178			
FT	NON-TER	Db	119 SMAPSSVTLQAGEDTGKPLGVEYAIKAHVGEDESDKGHKRSAVTLLTICKQYAPVSR	239			
SQ	SEQUENCE 431 AA; 47810 MW; 85C110785A815916 CRC64;	Qy	181 Q-PCTLVRKDFMMLSPGELEVLTDKOLYLHGERIGVNCIRNNSNKVKIKAWQGVDVVLFO	299			
Qy	6 KVFKKCAPNGKVTLYMGKRDFFDHDVSGVEPIDGIVVLDDEYIRDNRKVFGQIVCS	Db	240 DVVLFQNGSYRNTVASLETSEGCP10QGSSLQKWMYLPLISSNKRQRGIAALDGQIKRQD	297			
Db	66 EDLVLGLTFRKDLYLASEQIYPRPEKSDKQTKLQERLILKLGNSAIPFTFNIS	Qy	239 EVTMV-NAQFSKHAISLETREGCPITPGASFTKSFVPLASSNKRQRGIAALDGQIKRQD	299			
Qy	7 RVFKKSSNGKIKTIVYLGKRDFFDHDVSGVEPIDGIVVLDDEYIRDNRKVFGQIVCS	Db	300 OCTAATLIAQPD-ORDAFGVIIISYAVKVKLFLGALGELSAELPFLMHPKGT--KAK	356			
Db	126 SVTLQOGEDDNGDPCCGSYVYVLFAGESETDRTHRSTVTLGIRKIOAFTKQGQ	Qy	298 VNLLASSTLISEGKCPSDAMGIVVISYSLRKLNCGTIGLQDQTDVFKLMMNAPGSVER	357			
Qy	66 EDEVMGGLNFOKEIICLASEQIYPRPEKSDKQTKLQERLILKLGNSAIPFTFNIS	Db	357 VHADSDQADVETFRQDT--IDQOASVPE	383			
Db	125 SVSLQAPGDTGKPCGVDYELKAFAKVGESQEDKPHKRNSVRLAIRKIMYPSKLGHEQPSIE	Qy	358 VNALKKMKSIERHRYENSHVADDNNIVFE	387			
Qy	186 VRKDFMLSPGELELEVTLDKOLYLHGERIGVNCIRNNSNKVKIKAWQGVDVVLFO	Db					
Db	185 VSKEYILKPKNKHLEASLDKELYHIGESLSVNHANNSSKTVKKIKVSKLGEQPSIE	Qy					
Qy	245 TAOYKCTVAEVESEDGQVAPGFTLSKVFTLTPLLANKDKDQKGDQCLAST	Db					
Db	305 TLAQPDQDRAFTAFGVIIISYAVKVKLFLGALGELSAELPFLMHPKGT--KAK	Qy					
RESULT 9	306 TLAQPDQDRAFTAFGVIIISYAVKVKLFLGALGELSAELPFLMHPKGT--KAK	Db					
066gr6	305 TLAQPDQDRAFTAFGVIIISYAVKVKLFLGALGELSAELPFLMHPKGT--KAK	Qy					
ID	066GU6	PRELIMINARY;	PRT; 398 AA.				
AC	066GU6;						
DT	25-OCT-2004 (TREMBLrel. 28, Created)						
DT	25-OCT-2004 (TREMBLrel. 28, Last sequence update)						
DE	Arrestin 2-like protein Arr2.						
GN	Name=ARR2,						
OS	Anopheles gambiae						
OC	Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;						
OC	Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.						
RN	[1] NCBI_TaxID=180454;						
RP	SEQUENCE FROM N.A.						
RX	MEDLINE=23159591; PubMed=14966925;						
RA	Merrill C.E., Pitts R.J., Zwiebel L.J.;						
RT	"Molecular characterization of arrestin family members in the malaria vector mosquito, Anopheles gambiae,"						
RL	Insect Mol. Biol. 12:641-650 (2003).						
DR	EMBL; BK00996; DAA00881; -.						
DR	InterPro; IPR00698; Arrestin.						
DR	InterPro; IPR011022; Arrestin_C.						
DR	InterPro; IPR011021; Arrestin_N.						
DR	Pfam; PF02752; Arrestin_C; 1.						
DR	Pfam; PF00339; Arrestin_C; 1.						
DR	PRINTS; PR00309; Arrestin_N; 1.						
DR	ProDom; PD002099; Arrestin.						
DR	PROSITE; PS00295; Arrestin; 2.						
SQ	SEQUENCE 398 AA; 44536 MW; 73DD73FB34F01418 CRC64;						
Query Match	Best Local Similarity 51.8%; Score 1023; DB 2; Length 398;						
Qy	1 MWYNFKVKCACPNGKVTLYMGKRDFFDHDVSGVEPIDGIVVLDDEYIRDNRKVFGQIVCS						
Qy	1 MWYNFKVKCACPNGKVTLYMGKRDFFDHDVSGVEPIDGIVVLDDEYIRDNRKVFGQIVCS						

Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Wang Z.Y., Wasserman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodaget, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yer R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of *Drosophila melanogaster*." *Science* 287:2185-2195 (2000).

[12]

SEQUENCE FROM N.A.

RP MEDLINE=22426065; PubMed=12537568;

RX Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirska R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M., "Finishing a whole-genome shotgun: Release 3 of the *Drosophila melanogaster* euchromatic genome sequence." *Genome Biol.* 3:RESEARCH0079-RESEARCH0079 (2002).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=22426070; PubMed=12537573;

RX Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirska R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.; "The transposable elements of the *Drosophila melanogaster* euchromatin: a genomics perspective." *Genome Biol.* 3:RESEARCH0084-RESEARCH0084 (2002).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=22426069; PubMed=12537572;

RX Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P., RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A., RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M., RA Lewis S.E.; "Annotation of the *Drosophila melanogaster* euchromatic genome: a RT systematic review." *Genome Biol.* 3:RESEARCH0083-RESEARCH0083 (2002).

RN [5]

RP SEQUENCE FROM N.A.

RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Anamtidis P.G., Scherer S.E., Li P.W., Hoskins R.A., Gallo R.F., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D., RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L., RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra T., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Durbin R.J., Evangelista C.C., Ferrara S., Fleischmann W., RA Fosler C., Gabreliam A.B., Garg N.S., Gelbart W.M., Glasser K., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C., RA Jaijali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H., RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., RA

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Wan K.H., Doyce C., Baxter E.G., Heit G., Nelson C.R., Miklos G.I.G., Abril J.P., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., RA Ballieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., RA Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Durbin K.J., Evangelista C.C., Ferrara S., Fleischmann W., RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., RA Merkulov G., Milshina N.V., Nobarry C., Morris J., Moshrefi A., RA Mount S.M., Moy M., Murphy B., Murphy L., Muzyk D.M., Nelson D.L., RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J., RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., RA "The genome sequence of *Drosophila melanogaster*," RA Science 287:2185-2195 (2000). RA [3] RA RN [3] RA RP GENOME REANNOTATION. RA MEDLINE=2242609; PubMed=12537572; RA RA Mira S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P., RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M., RA Lewis S.E.; RA "Annotation of the *Drosophila melanogaster* euchromatic genome: a RA systematic review," Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002). RA [4] RA RP PHOSPHORYLATION, AND PROBABLE FUNCTION. RA MEDLINE=91282780; PubMed=1905538; RA RA Matsumoto H., Yamada T.; RA RT "Phosrestins I and II: arrestin homologs which undergo differential RT light-induced phosphorylation in the *Drosophila* photoreceptor *in vivo*," RT Biochem. Biophys. Res. Commun. 177:1306-1312 (1991). RA [5] RA RP PHOSPHORYLATION SITE SER-366. RA MEDLINE=94242441; PubMed=8185954; DOI=10.1016/0896-6273(94)90309-3; RA RA Matsumoto H., Kurien B.T., Takagi Y., Kahn E.S., Kinumi T., Komori N., RA RT "Phosrestin I undergoes the earliest light-induced phosphorylation by RT a calcium/calmodulin-dependent protein kinase in *Drosophila* RT photoreceptors," Neuron 12:997-1010 (1994). RA RL -1- FUNCTION: Probably plays an important role in the photoreceptor CC transduction. CC -1- TISSUE SPECIFICITY: Inner and outer segments, and the inner CC plexiform regions of the retina. CC -1- PTM: Phosphorylated upon light exposure. CC -1- SIMILARITY: Belongs to the arrestin family. CC

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CC ----- DR EMBL; M32141; AAA28833.1; -. DR EMBL; AE003554; AAF50380.1; -. DR PIR; A34856; A34856. DR HSSP; P17870; 1G4M. DR FLYBase; FBgn000121; Arr2. DR GO; GO:0005624; C:membrane fraction; IDA. DR GO; GO:0005625; C:soluble fraction; IDA. DR GO; GO:0016060; P:metarhodopsin inactivation; IMP. DR InterPro; IPR00698; Arrestin. DR IPR01022; Arrestin_C. DR InterPro; IPR011021; Arrestin_N. DR Pfam; PF02752; Arrestin_C; I. DR Pfam; PF00339; Arrestin_N; I. DR PRINTS; PR00309; ARRESTIN. DR PRODOM; PD002099; Arrestin; 2. DR PROSITE; PS00295; ARRESTINS; 1. DR KW phosphorylation; Sensory transduction; Vision. FT MOD RES 366 366 Phosphoserine (by CAMK). FT VARIANT 109 109 N -> S. FT CONFLICT 111 111 Y -> H (in Ref. 1). FT SEQUENCE 401 AA; 45028 MW; 12C776E0DA8F0D87 CRC64;

Query Match 49.8%; Score 982.5; DB 1; Length 401; Best Local Similarity 48.7%; Pred. No. 8.3e-68; Matches 191; Conservative 73; Mismatches 115; Indels 13; Gaps 6; RT RN

Qy 1 MVTNFVKFKKCAPNGKVLYMCKRDFVHDVSGVERIDGIVWLDDDEVYRDRNRYVFCQIVCS 60 Db 1 MVVSVVKVFKKATPNKGKVTFYLGRRDFIDHIDYCPVPGVIVVPEPDYLK-NRKVFGOLATT 59

Qy 61 FRYGREGEEVMGLNFQKELCLASEQIYPRPEKSDEQTKLQERLLKKLGNSNAIPFTFNIS 120 Db 60 YRYGREEDEVMGVKFSKELLICREBQIVPM-TNPNMEMTPMOKELVRLKGNSNAYPFTFFHP 118

Qy 121 PNAPSSVTLOQGEDDNGDPGCVSYVVKPAGESETDRTHRSTVTLGIRKIQFAPTKGQ 180 Db 119 PNSPSSVTLOQEGDDNGKPLGVETTIRAFVGQSEDDQRHRSMSVLVIKKQYAPLNGQ 178

Qy 181 Q-PCTLVKDFMLSPGELEVLTDKQLYLGERIGVNICIRNNSNKMKVKIKAMVQGV 239 Db 179 RLPSLVLVKGFTFSNGKISLVEVLDREIYHGKETAAVQVSNNSKSKVSKICFIVQHT 238

Qy 240 DVVLFQNGSYRNTVASLETSECCPIOPGSSLOKVMVLTPLLSSNKORRGIALDGOIKRD 299 Db 239 EITMV-NAQFSKHAQLETKEGPITPGANLTKTFYLIPLAANNKDRHGLADGHLD 297

Qy 300 OCTLASTTLLAQ-PDQDAFGVITISYAWKVKLPLGALGGELSAELPFVLMHPPKPGT---- 353 Db 298 VNLASSTMVQEGKSTGDAAGIVIVSYWSRIKUNCGTLLGEMQTDPFKLQLQAPGTEKKR 357

Qy 354 ---KAKVIHADSOADVETFRQDITDQASVDF 382 Db 358 SNAKKMKSIEQHRNVKGYYQDDDNIVFEDF 389

RESULT 14

ARRB_DROMI ID _ARRB_DROMI STANDARD; PRT; 401 AA.

AC P19108; DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Phosrestin I (Arrestin B) (Arrestin 2) (49 kDa arrestin-like protein).
GN Name=Arr2; Synonyms=ArrB;

Db	239	ITMV-NAQFSKRVQAQLETKEGCPTPGANLSTKTFYLIPLASNNKDRIGTALDGHILKDEDV	297
Qy	301	CLASTTLAQ-PDQDRAFTGVLISYAVKVKLFLGALGGELSAELPFVLMHPKPGT-----	353
Db	298	NLASSTMVQDGKSTGDAACGIVISYSVRILKNCGTLLGEGIQTDVPFKLLQPGSVEKRS	357
Qy	354	--KAKVIHADSOADQVETFRQPTIDQQASVDF	382
Db	358	NAMKKMKSIEQHRNTKGYYQDDDDNTIVFEDF	388

Search completed: February 9, 2005, 23:45:33
Job time : 66 secs

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OM protein - protein search, using SW model

Run on: February 9, 2005, 23:18:51 ; Search time 165 Seconds
 (without alignments)
 897.753 Million cell updates/sec

Title: US-10-056-405-2
 Perfect score: 1973
 Sequence: 1 MVYNPKVFKKCAPNGKVTLY.....ADVETFRQDTIDQQASVDFE 383
 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
 Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_16Dec04;*
 1: geneseqp1990s;*
 2: geneseqp2000s;*
 3: geneseqp2001s;*
 4: geneseqp2002s;*
 5: geneseqp2003s;*
 6: geneseqp2003bs;*
 7: geneseqp2004s;*
 8: geneseqp2004s;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1973	10.0	383	5 ABP52833
2	1973	10.0	383	7 ABR84476
3	1384	70.1	364	4 ABP52833 Anopheles
4	1384	70.1	364	8 ABP52833 Anopheles
5	1023	51.8	398	7 ABR84484
6	1002	50.8	470	4 ABP52833 Anopheles
7	982.5	49.9	401	4 ABP52833 Anopheles
8	907.5	46.0	410	4 ABP52833 Anopheles
9	903.5	45.8	418	4 ABP52833 Anopheles
10	903.5	45.8	452	5 ABP52833 Anopheles
11	900.5	45.6	418	5 ABP52833 Anopheles
12	900.5	45.6	418	8 ABP52833 Anopheles
13	897.5	45.5	418	4 ABP52833 Anopheles
14	890	45.1	369	4 ABP52833 Anopheles
15	885	44.9	409	4 ABP52833 Anopheles
16	885	44.9	409	4 ABP52833 Anopheles
17	885	44.9	409	7 ADE58183
18	885	44.9	409	7 ADE58179
19	885	44.9	409	7 ADN95251
20	880	44.6	409	4 AAG67784
21	874	44.3	360	6 ADA00637
22	874	44.3	495	6 ADA00637
23	869.5	44.1	410	5 ABG69496
24	869.5	44.1	410	7 ADE58177
25	869.5	44.1	410	7 ADE58181

ALIGNMENTS

RESULT 1	ABP52833	standard; protein; 383 AA.
ID	ABP52833	
XX	ABP52833;	
XX	01-NOV-2002	(first entry)
DT	XX	
DE	Anopheles gambiae arrestin 1 protein SEQ ID NO:2.	
XX		
KW	Anopheles gambiae; mosquito; olfactory gene; arrestin 1; pest control; odourant receptor; olfaction.	
KW		
OS	Anopheles gambiae.	
XX		
PN	WO200259274-A2.	
XX		
PD	01-AUG-2002.	
XX		
PP	01-AUG-2002; 2002WO-US002549.	
XX		
PR	26-JAN-2001; 2001US-0264649P.	
PR	24-JAN-2002; 2002US-00056405.	
XX		
PA	(UYVA-) UNIV VANDERBILT.	
XX		
PT	Zwiebel LJ;	
XX		
DR	WPI; 2002-627421/67.	
DR	N-PSDB; ABQ75102.	
XX		
PT	New mosquito olfaction polypeptides and polynucleotides, useful for mosquito management, i.e. controlling the pest and disease vectors, or for identifying pest control agents.	
PT		
PT	Claim 18; Fig 2; 96pp; English.	
PS		
XX		
The present invention describes a purified Anopheles gambiae olfaction polypeptide comprising a 383, 394, 380, 411, 412, 391, 157 or 401 residue amino acid sequence (see ABP52833 to ABP52840) (S1), a conservatively modified amino acid sequence of them, or a sequence of (S1) with at least 20 consecutive residues. Also described: (1) an isolated polynucleotide comprising: (a) a nucleotide sequence encoding the purified Anopheles gambiae olfaction polypeptide; or (b) a nucleotide sequence that hybridises under stringent conditions to a hybridisation probe comprising a 1964, 1239, 1142, 1236, 1194, 1176, 474 or 1206 nucleotide sequence (see ABQ75102 to ABQ75105 and ABQ75110 to ABQ75113) (S2), or its complement; and (2) a method for identifying an agent that binds to	Adr23187 Yellow fl Adr23188 Green flu Adr23186 Yellow fl Adr24049 Bacterial Adg67783 Amino aci Aam78763 Human pro Aag67782 Amino aci Adq14327 Human ret Adr41708 Protein s Aam79747 Human pro Ada00634 Human bet Ada00636 Human bet Add27197 Human adi Aag73899 Human col Abb58949 Drosophil Abb42223 Peptide #	

CC mosquito olfaction molecules comprising: (a) providing an isolated mosquito olfaction molecule; (b) contacting a test agent with the presence of specific binding identified by the isolated mosquito olfaction molecule; and (c) detecting specific binding for mosquito management, i.e. controlling the test agent as a mosquito modulate arrestin-odourant agents. The present invention of screening this pest and disease vector. A pest control agents. The present invention is useful for identifying arrestin 1 from the present invention

SQ Sequence 383 AA;

Query Match

Best Local Similarity

100.0%; Score 1973; DB 5; Length 383;

Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVYNFKVKKKCAGNPKVLYMGRDFDVHVSVERIDGIVVLDDEYIRDNRKVFQIVCS 60

QY 61 FRYGRREDEVMLNFOKEELCLASEQIYPRPEKSDEKQTKLQERLKKLGNSNAIPFTENIS 120

QY 121 PNAPSSVTLQQGEDDNGDPGCVSYVYKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQ 180

QY 121 PNAPSSVTLQQGEDDNGDPGCVSYVYKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQ 180

Db 181 QPCTLVRKDFMLSPGELELEVTLDKOLYLGERICGNICIRNNSNKMKIKAMVQGV 240

QY 241 VVLFONGSYRNTVASLETSEGCPQPGSSLQKVMVLTPLISSNKORRGIAIDGQIKRQDQ 300

Db 241 VVLFONGSYRNTVASLETSEGCPQPGSSLQKVMVLTPLISSNKORRGIAIDGQIKRQDQ 240

QY 301 CLASTTLLAQDQDRAFTGVIVSYAVKVKLFLGALGGELSAELPFVLMHPKPGTKAKVTHA 360

Db 301 CLASTTLLAQDQDRAFTGVIVSYAVKVKLFLGALGGELSAELPFVLMHPKPGTKAKVTHA 360

QY 361 DSQADVEFRRDTIDQASVDFE 383

Db 361 DSQADVEFRRDTIDQASVDFE 383

RESULT 2
ABR84476
ID ABR84476 standard; protein: 383 AA.
AC ABR84476;
XX DT 15-JAN-2004 (first entry)
DE Mosquito olfaction molecule, arrestin 1.
XX Arrestin 1; mosquito; olfaction; insecticide; antimalarial.
OS Anopheles gambiae.
PN WO2003076590-A2.
XX PD 18-SEP-2003.
XX PR 08-MAR-2002; 2002US-00094240.
PA (UYVA-) UNIV VANDERBILT.
PI Zwiebel LJ;
XX

DR WPI; 2003-72231/68.
DR N-PSDB; ACP79716.

PT New mosquito arrestin 1 and 2 genes and polypeptides, useful for identifying mosquito olfaction molecule binding compounds which reduce the ability of mosquitoes to locate sources of bloodmeal, e.g. humans.

CC The present sequence is the protein sequence of arrestin 1, a novel polypeptides and the nucleic acids encoding them. These are arrestin 1 and 2 and odorant receptor molecules 1-7. The odorant receptors function in a ligand-induced signal transduction cascade. Arrestin functions to inhibit the activation of mosquito olfaction and arrestin as an 'off', switch for the odorant receptors act as an 'on' switch, with the operation of the mosquito olfactory system, particularly by reducing their ability to locate sources of mosquitoes, particularly by reducing their ability to locate

Sequence 383 AA;

Query Match

Best Local Similarity

100.0%; Score 1973; DB 7; Length 383;

Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVYNFKVKKKCAGNPKVLYMGRDFDVHVSVERIDGIVVLDDEYIRDNRKVFQIVCS 60

QY 61 FRYGRREDEVMLNFOKEELCLASEQIYPRPEKSDEKQTKLQERLKKLGNSNAIPFTENIS 120

QY 121 PNAPSSVTLQQGEDDNGDPGCVSYVYKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQ 180

QY 121 PNAPSSVTLQQGEDDNGDPGCVSYVYKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQ 180

Db 181 QPCTLVRKDFMLSPGELELEVTLDKOLYLGERICGNICIRNNSNKMKIKAMVQGV 240

QY 241 VVLFONGSYRNTVASLETSEGCPQPGSSLQKVMVLTPLISSNKORRGIAIDGQIKRQDQ 300

Db 480 241 VVLFONGSYRNTVASLETSEGCPQPGSSLQKVMVLTPLISSNKORRGIAIDGQIKRQDQ 240

QY 301 CLASTTLLAQDQDRAFTGVIVSYAVKVKLFLGALGGELSAELPFVLMHPKPGTKAKVTHA 360

Db 301 CLASTTLLAQDQDRAFTGVIVSYAVKVKLFLGALGGELSAELPFVLMHPKPGTKAKVTHA 360

QY 361 DSQADVEFRRDTIDQASVDFE 383

Db 361 DSQADVEFRRDTIDQASVDFE 383

RESULT 3
ABB61736
ID ABB61736 standard; protein: 364 AA.
AC ABB61736;
XX DT 26-MAR-2002 (first entry)
DE Drosophila melanogaster polypeptide SEQ ID NO 12000.
XX KW Drosophila; developmental biology; cell signalling; insecticide;
OS Drosophila melanogaster.

PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PR 23-MAR-2001; 2001WO-US009231.
 XX
 PR 23-MAR-2000; 2000US-0191637P.
 XX
 PR 11-JUL-2000; 2000US-00614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI; 2001-656860/75.
 DR N-PSDB; ABL05839.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from *Drosophila* and for elucidating cell signaling and cell-cell interactions.
 PT
 XX
 PS Disclosure; SEQ ID NO 12000; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from *Drosophila*. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL3051), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB5737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://ftp.wipo.int/pub/published_pct_sequence
 CC
 XX
 SQ Sequence 364 AA;

Query Match 70.1%; Score 1384; DB 4; Length 364;
 Best Local Similarity 70.3%; Pred. No. 1.5e-135;
 Matches 258; Conservative 51; Mismatches 54; Indels 4; Gaps 2;

Qy 1 MVVNFKVKKKCAGNGKVTLYMGRKDFDVFHSGVVERIDGIVWLDEYIRDNRKVFGQIVCS 60
 Db 1 MVVNFKVKKKCSPNNMITLYMRRDFVDSVTQVEPIDGIVVLDEYVRQNRKIFVOLVCN 60

Qy 61 FRYGREEDEVMGLNFOKEKLCLASEQIYPRPEKSDEQTKLQERLLKKLGSNAIPFTNIS 120
 Db 61 FRYGREDDEMIGLRFOKELTIVSQQCP-PQKDIQLTQMRERLLKKLGSNAIPFTNIS 119

Qy 121 PNAPSSVTLQOGEDDNGDPGGSVYVVKIFAGESETDRTHRSTVTLGIRKIQAPTKQGQ 180
 Db 120 PSSPASVVLQOKASDESQPCGVQYFVKIFGDSDCDRSHRRSTINLGIRKQYAPTKQGI 179

Qy 181 QPCTLVRKDFMLSPGELELETVTLDKQLYLHGERIGVNICIRNNSNKMKKKIKAMVQOGVD 240
 Db 180 QPCTVVRKDFLLSPGELELETVTLDKQLYHGEKISVNICVRNNSNKVKIKAMVQOGVD 239

Qy 241 VVLFQONGSYRNTVASLETSECCPIQPGSSLOKVMYLTPLLSNKQRRGIALDQIKRDO 300
 Db 240 VVLFQONGQFRNTIAFMETSECCPILNPGSSLOKVMYLVPTLVANCDRAGIAVEGDIKKDT 299

Qy 301 CLASTILLAOPDQDAFGVIIISAVKVKLFLGALGELSAELPFVLMHPKPGTKAKVHIA 360
 Db 300 ALASTTLIASQDARDAFGVIIISAVKVKLFLGALGELCAELPFVLMHPKPSRKAQL-- 356

Qy 361 DSQADVE 367
 Db 357 EAEGSIE 363

XX
 SQ Sequence 364 AA;

Query Match 70.1%; Score 1384; DB 8; Length 364;
 Best Local Similarity 70.3%; Pred. No. 1.5e-135;
 Matches 258; Conservative 51; Mismatches 54; Indels 4; Gaps 2;

Qy 1 MVVNFKVKKKCAGNGKVTLYMGRKDFDVFHSGVVERIDGIVWLDEYIRDNRKVFGQIVCS 60
 Db 1 MVVNFKVKKKCSPNNMITLYMRRDFVDSVTQVEPIDGIVVLDEYVRQNRKIFVOLVCN 60

Qy 61 FRYGREEDEVMGLNFOKEKLCLASEQIYPRPEKSDEQTKLQERLLKKLGSNAIPFTNIS 120
 Db 61 FRYGREDDEMIGLRFOKELTIVSQQCP-PQKDIQLTQMRERLLKKLGSNAIPFTNIS 119

Qy 121 PNAPSSVTLQOGEDDNGDPGGSVYVVKIFAGESETDRTHRSTVTLGIRKIQAPTKQGQ 180
 Db 120 PSSPASVVLQOKASDESQPCGVQYFVKIFGDSDCDRSHRRSTINLGIRKQYAPTKQGI 179

Qy 181 QPCTLVRKDFMLSPGELELETVTLDKQLYLHGERIGVNICIRNNSNKMKKKIKAMVQOGVD 240
 Db 180 QPCTVVRKDFLLSPGELELETVTLDKQLYHGEKISVNICVRNNSNKVKIKAMVQOGVD 239

Qy 241 VVLFQONGSYRNTVASLETSECCPIQPGSSLOKVMYLTPLLSNKQRRGIALDQIKRDO 300
 Db 240 VVLFQONGQFRNTIAFMETSECCPILNPGSSLOKVMYLVPTLVANCDRAGIAVEGDIKKDT 299

Qy 301 CLASTILLAOPDQDAFGVIIISAVKVKLFLGALGELSAELPFVLMHPKPGTKAKVHIA 360
 AC ADQ89588;

RESULT 4
 ADQ89588
 ID ADQ89588 standard; protein; 364 AA.
 XX
 AC ADQ89588;

Db	3 00 ALASTTLIASQDARDAGFGITVSYAVKVKLFLGALGGELCAELPPFILMHPKPSRAQL---	Qy	3 61 DSQADVE 367	Db	357 BAECSIE 363
RESULT 5		Qy	121 PNAPSSVTLOOGEDDNGDPCGVSYVTKIPAGESETDRTHRSTVTLGIRKIQAPTKQGQ 180		
ABR84484		Db	119 SMAPSSVTIQAGEDDDTGKPLGVYAIKAHVGEDESDKGHKRSAVTILKQLQVAPVSRG 178		
ID		Qy	181 Q-PCTILVRKDFMLSPGELEVTLDKQLYLHGERIGNVICIRNNSNKQVCKAWVQGV 239		
XX		Db	179 RLPSLVLVKGFTFSQKINLEVTLDREIVYHGEKAAANIVVTRNSRKTIVSICKFVQHC 238		
AC		Qy	240 DVLFQNGSYRNTVASLSETSEGCPQPGSSLQKUMLTPLISSNKQRRGIALDQIKRQD 299		
XX		Db	239 EVTMV-NAQFSKHLASLETREGCPITPGASFTKSFVPLASSNKDRRGIALDGHLIKED 297		
DT		Qy	300 QCASTRULLAQPD-QRDAFGVIIYAVKVKLFLGALGGELSAELPFVLMRPGT--KAK 356		
15-JAN-2004	(first entry)	Db	298 VNLAASSTLISEGKCPSPDAMGIVIVSYSLRVKLNCGTLLGEIQLTDVPPKLMNPAGSVER 357		
XX		Qy	357 VTHADSQADVEFRQDT--IDQQASVDFE 383		
DE		Db	358 VNALKKMKSIERHRYENSHADDNNIVFE 387		
Mosquito olfaction molecule, arrestin 2.					
KW		Qy	121 PNAPSSVTLOOGEDDNGDPCGVSYVTKIPAGESETDRTHRSTVTLGIRKIQAPTKQGQ 180		
XX		Db	119 SMAPSSVTIQAGEDDDTGKPLGVYAIKAHVGEDESDKGHKRSAVTILKQLQVAPVSRG 178		
OS		Qy	181 Q-PCTILVRKDFMLSPGELEVTLDKQLYLHGERIGNVICIRNNSNKQVCKAWVQGV 239		
Anopheles gambiae.		Db	179 RLPSLVLVKGFTFSQKINLEVTLDREIVYHGEKAAANIVVTRNSRKTIVSICKFVQHC 238		
XX		Qy	240 DVLFQNGSYRNTVASLSETSEGCPQPGSSLQKUMLTPLISSNKQRRGIALDQIKRQD 299		
FH		Db	239 EVTMV-NAQFSKHLASLETREGCPITPGASFTKSFVPLASSNKDRRGIALDGHLIKED 297		
Key		Qy	300 QCASTRULLAQPD-QRDAFGVIIYAVKVKLFLGALGGELSAELPFVLMRPGT--KAK 356		
FT		Db	298 VNLAASSTLISEGKCPSPDAMGIVIVSYSLRVKLNCGTLLGEIQLTDVPPKLMNPAGSVER 357		
Misc-difference 152		Qy	357 VTHADSQADVEFRQDT--IDQQASVDFE 383		
XX		Db	358 VNALKKMKSIERHRYENSHADDNNIVFE 387		
PN		Qy	121 PNAPSSVTLOOGEDDNGDPCGVSYVTKIPAGESETDRTHRSTVTLGIRKIQAPTKQGQ 180		
XX		Db	119 SMAPSSVTIQAGEDDDTGKPLGVYAIKAHVGEDESDKGHKRSAVTILKQLQVAPVSRG 178		
PD		Qy	181 Q-PCTILVRKDFMLSPGELEVTLDKQLYLHGERIGNVICIRNNSNKQVCKAWVQGV 239		
XX		Db	179 RLPSLVLVKGFTFSQKINLEVTLDREIVYHGEKAAANIVVTRNSRKTIVSICKFVQHC 238		
PF		Qy	240 DVLFQNGSYRNTVASLSETSEGCPQPGSSLQKUMLTPLISSNKQRRGIALDQIKRQD 299		
XX		Db	239 EVTMV-NAQFSKHLASLETREGCPITPGASFTKSFVPLASSNKDRRGIALDGHLIKED 297		
10-MAR-2003		Qy	300 QCASTRULLAQPD-QRDAFGVIIYAVKVKLFLGALGGELSAELPFVLMRPGT--KAK 356		
XX		Db	298 VNLAASSTLISEGKCPSPDAMGIVIVSYSLRVKLNCGTLLGEIQLTDVPPKLMNPAGSVER 357		
PR		Qy	357 VTHADSQADVEFRQDT--IDQQASVDFE 383		
XX		Db	358 VNALKKMKSIERHRYENSHADDNNIVFE 387		
(URVA-) UNIV VANDERBILT.		Qy	121 PNAPSSVTLOOGEDDNGDPCGVSYVTKIPAGESETDRTHRSTVTLGIRKIQAPTKQGQ 180		
XX		Db	119 SMAPSSVTIQAGEDDDTGKPLGVYAIKAHVGEDESDKGHKRSAVTILKQLQVAPVSRG 178		
PA		Qy	181 Q-PCTILVRKDFMLSPGELEVTLDKQLYLHGERIGNVICIRNNSNKQVCKAWVQGV 239		
XX		Db	179 RLPSLVLVKGFTFSQKINLEVTLDREIVYHGEKAAANIVVTRNSRKTIVSICKFVQHC 238		
PI		Qy	240 DVLFQNGSYRNTVASLSETSEGCPQPGSSLQKUMLTPLISSNKQRRGIALDQIKRQD 299		
XX		Db	239 EVTMV-NAQFSKHLASLETREGCPITPGASFTKSFVPLASSNKDRRGIALDGHLIKED 297		
Zwiebel LJ;		Qy	300 QCASTRULLAQPD-QRDAFGVIIYAVKVKLFLGALGGELSAELPFVLMRPGT--KAK 356		
DR		Db	298 VNLAASSTLISEGKCPSPDAMGIVIVSYSLRVKLNCGTLLGEIQLTDVPPKLMNPAGSVER 357		
N-PSDB; ACF/9731.		Qy	357 VTHADSQADVEFRQDT--IDQQASVDFE 383		
XX		Db	358 VNALKKMKSIERHRYENSHADDNNIVFE 387		
PT		Qy	121 PNAPSSVTLOOGEDDNGDPCGVSYVTKIPAGESETDRTHRSTVTLGIRKIQAPTKQGQ 180		
XX		Db	119 SMAPSSVTIQAGEDDDTGKPLGVYAIKAHVGEDESDKGHKRSAVTILKQLQVAPVSRG 178		
PT		Qy	181 Q-PCTILVRKDFMLSPGELEVTLDKQLYLHGERIGNVICIRNNSNKQVCKAWVQGV 239		
XX		Db	179 RLPSLVLVKGFTFSQKINLEVTLDREIVYHGEKAAANIVVTRNSRKTIVSICKFVQHC 238		
PS		Qy	240 DVLFQNGSYRNTVASLSETSEGCPQPGSSLQKUMLTPLISSNKQRRGIALDQIKRQD 299		
Claim 16; Fig 12b; 101pp; English.		Db	239 EVTMV-NAQFSKHLASLETREGCPITPGASFTKSFVPLASSNKDRRGIALDGHLIKED 297		
CC		Qy	300 QCASTRULLAQPD-QRDAFGVIIYAVKVKLFLGALGGELSAELPFVLMRPGT--KAK 356		
CC		Db	298 VNLAASSTLISEGKCPSPDAMGIVIVSYSLRVKLNCGTLLGEIQLTDVPPKLMNPAGSVER 357		
CC		Qy	357 VTHADSQADVEFRQDT--IDQQASVDFE 383		
CC		Db	358 VNALKKMKSIERHRYENSHADDNNIVFE 387		
CC		Qy	121 PNAPSSVTLOOGEDDNGDPCGVSYVTKIPAGESETDRTHRSTVTLGIRKIQAPTKQGQ 180		
CC		Db	119 SMAPSSVTIQAGEDDDTGKPLGVYAIKAHVGEDESDKGHKRSAVTILKQLQVAPVSRG 178		
CC		Qy	181 Q-PCTILVRKDFMLSPGELEVTLDKQLYLHGERIGNVICIRNNSNKQVCKAWVQGV 239		
CC		Db	179 RLPSLVLVKGFTFSQKINLEVTLDREIVYHGEKAAANIVVTRNSRKTIVSICKFVQHC 238		
CC		Qy	240 DVLFQNGSYRNTVASLSETSEGCPQPGSSLQKUMLTPLISSNKQRRGIALDQIKRQD 299		
CC		Db	239 EVTMV-NAQFSKHLASLETREGCPITPGASFTKSFVPLASSNKDRRGIALDGHLIKED 297		
CC		Qy	300 QCASTRULLAQPD-QRDAFGVIIYAVKVKLFLGALGGELSAELPFVLMRPGT--KAK 356		
CC		Db	298 VNLAASSTLISEGKCPSPDAMGIVIVSYSLRVKLNCGTLLGEIQLTDVPPKLMNPAGSVER 357		
CC		Qy	357 VTHADSQADVEFRQDT--IDQQASVDFE 383		
CC		Db	358 VNALKKMKSIERHRYENSHADDNNIVFE 387		
CC		Qy	121 PNAPSSVTLOOGEDDNGDPCGVSYVTKIPAGESETDRTHRSTVTLGIRKIQAPTKQGQ 180		
CC		Db	119 SMAPSSVTIQAGEDDDTGKPLGVYAIKAHVGEDESDKGHKRSAVTILKQLQVAPVSRG 178		
CC		Qy	181 Q-PCTILVRKDFMLSPGELEVTLDKQLYLHGERIGNVICIRNNSNKQVCKAWVQGV 239		
CC		Db	179 RLPSLVLVKGFTFSQKINLEVTLDREIVYHGEKAAANIVVTRNSRKTIVSICKFVQHC 238		
CC		Qy	240 DVLFQNGSYRNTVASLSETSEGCPQPGSSLQKUMLTPLISSNKQRRGIALDQIKRQD 299		
CC		Db	239 EVTMV-NAQFSKHLASLETREGCPITPGASFTKSFVPLASSNKDRRGIALDGHLIKED 297		
CC		Qy	300 QCASTRULLAQPD-QRDAFGVIIYAVKVKLFLGALGGELSAELPFVLMRPGT--KAK 356		
CC		Db	298 VNLAASSTLISEGKCPSPDAMGIVIVSYSLRVKLNCGTLLGEIQLTDVPPKLMNPAGSVER 357		
CC		Qy	357 VTHADSQADVEFRQDT--IDQQASVDFE 383		
CC		Db	358 VNALKKMKSIERHRYENSHADDNNIVFE 387		
CC		Qy	121 PNAPSSVTLOOGEDDNGDPCGVSYVTKIPAGESETDRTHRSTVTLGIRKIQAPTKQGQ 180		
CC		Db	119 SMAPSSVTIQAGEDDDTGKPLGVYAIKAHVGEDESDKGHKRSAVTILKQLQVAPVSRG 178		
CC		Qy	181 Q-PCTILVRKDFMLSPGELEVTLDKQLYLHGERIGNVICIRNNSNKQVCKAWVQGV 239		
CC		Db	179 RLPSLVLVKGFTFSQKINLEVTLDREIVYHGEKAAANIVVTRNSRKTIVSICKFVQHC 238		
CC		Qy	240 DVLFQNGSYRNTVASLSETSEGCPQPGSSLQKUMLTPLISSNKQRRGIALDQIKRQD 299		
CC		Db	239 EVTMV-NAQFSKHLASLETREGCPITPGASFTKSFVPLASSNKDRRGIALDGHLIKED 297		
CC		Qy	300 QCASTRULLAQPD-QRDAFGVIIYAVKVKLFLGALGGELSAELPFVLMRPGT--KAK 356		
CC		Db	298 VNLAASSTLISEGKCPSPDAMGIVIVSYSLRVKLNCGTLLGEIQLTDVPPKLMNPAGSVER 357		
CC		Qy	357 VTHADSQADVEFRQDT--IDQQASVDFE 383		
CC		Db	358 VNALKKMKSIERHRYENSHADDNNIVFE 387		
CC		Qy	121 PNAPSSVTLOOGEDDNGDPCGVSYVTKIPAGESETDRTHRSTVTLGIRKIQAPTKQGQ 180		
CC		Db	119 SMAPSSVTIQAGEDDDTGKPLGVYAIKAHVGEDESDKGHKRSAVTILKQLQVAPVSRG 178		
CC		Qy	181 Q-PCTILVRKDFMLSPGELEVTLDKQLYLHGERIGNVICIRNNSNKQVCKAWVQGV 239		
CC		Db	179 RLPSLVLVKGFTFSQKINLEVTLDREIVYHGEKAAANIVVTRNSRKTIVSICKFVQHC 238		
CC		Qy	240 DVLFQNGSYRNTVASLSETSEGCPQPGSSLQKUMLTPLISSNKQRRGIALDQIKRQD 299		
CC		Db	239 EVTMV-NAQFSKHLASLETREGCPITPGASFTKSFVPLASSNKDRRGIALDGHLIKED 297		
CC		Qy	300 QCASTRULLAQPD-QRDAFGVIIYAVKVKLFLGALGGELSAELPFVLMRPGT--KAK 356		
CC		Db	298 VNLAASSTLISEGKCPSPDAMGIVIVSYSLRVKLNCGTLLGEIQLTDVPPKLMNPAGSVER 357		
CC		Qy	357 VTHADSQADVEFRQDT--IDQQASVDFE 383		
CC		Db	358 VNALKKMKSIERHRYENSHADDNNIVFE 387		
CC		Qy	121 PNAPSSVTLOOGEDDNGDPCGVSYVTKIPAGESETDRTHRSTVTLGIRKIQAPTKQGQ 180		
CC		Db	119 SMAPSSVTIQAGEDDDTGKPLGVYAIKAHVGEDESDKGHKRSAVTILKQLQVAPVSRG 178		
CC		Qy	181 Q-PCTILVRKDFMLSPGELEVTLDKQLYLHGERIGNVICIRNNSNKQVCKAWVQGV 239		
CC		Db	179 RLPSLVLVKGFTFSQKINLEVTLDREIVYHGEKAAANIVVTRNSRKTIVSICKFVQHC 238		
CC		Qy	240 DVLFQNGSYRNTVASLSETSEGCPQPGSSLQKUMLTPLISSNKQRRGIALDQIKRQD 299		
CC		Db	239 EVTMV-NAQFSKHLASLETREGCPITPGASFTKSFVPLASSNKDRRGIALDGHLIKED 297		
CC		Qy	300 QCASTRULLAQPD-QRDAFGVIIYAVKVKLFLGALGGELSAELPFVLMRPGT--KAK 356		
CC		Db	298 VNLAASSTLISEGKCPSPDAMGIVIVSYSLRVKLNCGTLLGEIQLTDVPPKLMNPAGSVER 357		
CC		Qy	357 VTHADSQADVEFRQDT--IDQQASVDFE 383		
CC		Db	358 VNALKKMKSIERHRYENSHADDNNIVFE 387		
CC		Qy	121 PNAPSSVTLOOGEDDNGDPCGVSYVTKIPAGESETDRTHRSTVTLGIRKIQAPTKQGQ 180		
CC		Db	119 SMAPSSVTIQAGEDDDTGKPLGVYAIKAHVGEDESDKGHKRSAVTILKQLQVAPVSRG 178		
CC		Qy	181 Q-PCTILVRKDFMLSPGELEVTLDKQLYLHGERIGNVICIRNNSNKQVCKAWVQGV 239		
CC		Db	179 RLPSLVLVKGFTFSQKINLEVTLDREIVYHGEKAAANIVVTRNSRKTIVSICKFVQHC 238		
CC		Qy	240 DVLFQNGSYRNTVASLSETSEGCPQPGSSLQKUMLTPLISSNKQRRGIALDQIKRQD 299		
CC		Db	239 EVTMV-NAQFSKHLASLETREGCPITPGASFTKSFVPLASSNKDRRGIALDGHLIKED 297		
CC		Qy	300 QCASTRULLAQPD-QRDAFGVIIYAVKVKLFLGALGGELSAELPFVLMRPGT--KAK 356		
CC		Db	298 VNLAASSTLISEGKCPSPDAMGIVIVSYSLRVKLNCGTLLGEIQLTDVPPKLMNPAGSVER 357		
CC		Qy	357 VTHADSQADVEFRQDT--IDQQASVDFE 383		
CC		Db	358 VNALKKMKSIERHRYENSHADDNNIVFE 387		
CC		Qy	121 PNAPSSVTLOOGEDDNGDPCGVSYVTKIPAGESETDRTHRSTVTLGIRKIQAPTKQGQ 180		
CC		Db	119 SMAPSSVTIQAGEDDDTGKPLGVYAIKAHVGEDESDKGHKRSAVTILKQLQVAPVSRG 178		
CC		Qy	181 Q-PCTILVRKDFMLSPGELEVTLDKQLYLHGERIGNVICIRNNSNKQVCKAWVQGV 239		
CC		Db	179 RLPSLVLVKGFTFSQKINLEVTLDREIVYHGEKAAANIVVTRNSRKTIVSICKFVQHC 238		
CC		Qy	240 DVLFQNGSYRNTVASLSETSEGCPQPGSSLQKUMLTPLISSNKQRRGIALDQIKRQD 299		
CC		Db	239 EVTMV-NAQFSKHLASLETREGCPITPGASFTKSFVPLASSNKDRRGIALDGHLIKED 297		
CC		Qy	300 QCASTRULLAQPD-QRDAFGVIIYAVKVKLFLGALGGELSAELPFVLMRPGT--KAK 356		
CC		Db	298 VNLAASSTLISEGKCPSPDAMGIVIVSYSLRVKLNCGTLLGEIQLTDVPPKLMNPAGSVER 357		
CC		Qy	357 VTHADSQADVEFRQDT--IDQQASVDFE 383		
CC		Db	358 VNALKKMKSIERHRYENSHADDNNIVFE 387		
CC		Qy	121 PNAPSSVTLOOGEDDNGDPCGVSYVTKIPAGESETDRTHRSTVTLGIRKIQAPTKQGQ 180		
CC		Db	119 SMAPSSVTIQAGEDDDTGKPLGVYAIKAHVGEDESDKGHKRSAVTILKQLQVAPVSRG 178		
CC		Qy	181 Q-PCTILVRKDFMLSPGELEVTLDKQLYLHGERIGNVICIRNNSNKQVCKAWVQGV 239		
CC		Db	179 RLPSLVLVKGFTFSQKINLEVTLDREIVYHGEKAAANIVVTRNSRKTIVSICKFVQHC 238		
CC		Qy	240 DVLFQNGSYRNTVASLSETSEGCPQPGSSLQKUMLTPLISSNKQRRGIALDQIKRQD 299		
CC		Db	239 EVTMV-NAQFSKHLASLETREGCPITPGASFTKSFVPLASSNKDRRGIALDGHLIKED 297		
CC		Qy	300 QCASTRULLAQPD-QRDAFGVIIYAVKVKLFLGALGGELSAELPFVLMRPGT--KAK 356		
CC		Db			

DR WPI; 2001-602637/68.

XX

PT

DE Amino acid sequence of bovine beta-arrestin 1A.

XX

KW

DE Amino acid sequence of bovine beta-arrestin 1A.

XX

KW

DE Amino acid sequence of bovine beta-arrestin 1A.

XX

KW

DE Amino acid sequence of bovine beta-arrestin 1A.

XX

KW

DE Amino acid sequence of bovine beta-arrestin 1A.

XX

KW

Db 126 SVTLQPGPEDTGKACGVYEVKAFCAGENLEEKIHKRNSVRLVIRKQYAPERPGPQOPTAE 185
 Qy 186 VRKDFMLSPGELELETLDKOLYLHGERIGVNICIRNNSNKMKKKIKAMVQGVDVLFQ 245
 CC compound isolated by the method is useful for treating and preventing
 Db 186 TTRQFLMSDKPLHLEASLDKEIYHGEPIISVNVTNNTKTKIKISVRQYADICLFN 245
 Qy 246 NGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPPLLSNNKORRGIALEQIKRQDQCLAST 305
 CC invention, used as the bait protein in the yeast two- hybrid assay
 Db 246 TAQYKCPVAMEEADD--TVAPSSTFCKVLTTPFLANNREKGLADGKLUKHEDTNLASS 303
 Qy 306 TLLAQPDQDRAFTGVIISYAVKVKLFL--GALGGEELSA----ELPFVLMHPPKGTK--A 355
 CC
 Db 304 TLLREGANREILGILIVSYKVVKVVLVSRGGGLGDLASSDVAVELPFTLMHPPKKEEPPHR 363
 Qy 356 KVIHADSDQADVETFQDFTID 375
 Db 364 EVPEHETPVDTNLIEDTND 383

RESULT 10

ABG69495 ID ABG69495 standard; protein; 452 AA.
 XX
 AC ABG69495;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Rat bait protein beta arrestin 1.
 XX
 KW Rat; yeast two-hybrid assay; adipocyte; bait protein; NIDDM; non-insulin diabetes mellitus; obesity; selected interacting domain; SID; protein-protein interaction map; PIM; anorectic; metabolic disorder.
 XX
 OS Rattus sp.
 XX
 PN WO200253726-A2.
 XX
 PD 11-JUL-2002.
 XX
 PR 28-DEC-2001; 2001WO-EP015423.
 XX
 PR 02-JAN-2001; 2001US-0259377P.
 XX
 PA (HYBR-) HYBRIGENICS.
 PA (CNRS) CENT NAT RECH SCI.
 XX
 PI Legrain P, Marullo S, Jockers R;
 XX
 DR N-PSDB; ABS51031.
 XX
 PT Novel complex of protein-protein interactions in adipocyte cells for identifying compounds that modulate the protein-protein interactions and useful for treating obesity and metabolic disorders.
 XX
 PS Claim 1; Page 52; 125pp; English.
 XX
 CC The invention relates to a complex of protein-protein interactions (forming a protein-protein interaction map, PIM) in adipocyte cells as defined in the specification, or polynucleotides in adipocytes encoding the polypeptides. Also included are a recombinant cell expressing the interacting polypeptides and a method of selecting a modulating compound in adipocyte cells, by cultivating a recombinant host cell on a selective medium containing a modulating compound and a reporter gene, the expression of which is toxic for the recombinant host cell which is transformed with two vectors, where the first vector comprises a polynucleotide encoding a first hybrid polypeptide and DNA binding domain and the second vector comprising a polynucleotide encoding a second hybrid polypeptide and an activating domain that activates the toxic reporter gene, when the first and second hybrid polypeptides interact and selecting the modulating compound which inhibits the growth of the recombinant host cell (i.e. using the yeast two-hybrid system). The complexes are useful for identifying compounds that modulate the protein-
 CC protein interactions and useful for treating obesity and metabolic disorders e.g. non-insulin dependent diabetes mellitus, NIDDM. The compound isolated by the method is useful for treating and preventing obesity or metabolic diseases. The interactions between the proteins of the complex further define a set of selected interacting domains, SID. The present sequence represents a member of the protein complex of the invention, used as the bait protein in the yeast two- hybrid assay

SQ Sequence 452 AA;

Query Match 45.8%; Score 903.5; DB 5; Length 452;
 Best Local Similarity 47.1%; Pred: No. 4.7e-85;
 Matches 179; Conservative 76; Mismatches 112; Indels 13; Gaps 5;

Db 66 EDEEVMLNFOKECLASEQIYPRPEKSDKEQTKLQERLKKLGSNAIPFTFNISPNAES 125
 Qy 7 RVFKKASPNQKLTVYLGKRRDFVHDHIDLVEPVDPGVVLVDPPEYKLE-RRVYVTLCAFYGR 65

Db 126 SVTLQPGPEDTGKACGVYEVKAFCAGENLEEKIHKRNSVRLVIRKQYAPERPGPQOPTAE 185
 Qy 186 VRKDFMLSPGELELETLDKOLYLHGERIGVNICIRNNSNKMKKKIKAMVQGVDVLFQ 245
 Qy 246 NGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPPLLSNNKORRGIALEQIKRQDQCLAST 305
 Db 304 TLLREGANREILGILIVSYKVVKVVLVSRGGGLGDLASSDVAVELPFTLMHPPKKEEPPHR 363
 Qy 356 KVIHADSDQADVETFQDFTID 375
 Db 364 EVPEHETPVDTNLIEDTND 383

RESULT 11

ABG70174 ID ABG70174 standard; protein; 418 AA.
 XX
 AC ABG70174;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human prey protein for Shigella ipaH9.8 #4.
 XX
 KW Prey protein; ospB; ospD1; ipaD; ipaC; ipaH9.8; ospG; ospC1; Shigella; shigellosis; bacillary dysentery; antibacterial; yeast two-hybrid system; protein-protein interaction; SID; selected interacting domain; human.
 XX
 OS Homo sapiens.
 XX
 PN WO200257303-A2.
 XX
 PD 25-JUL-2002.
 XX
 PP 11-JAN-2002; 2002WO-EP000777.
 XX
 PR 12-JAN-2001; 2001US-0261130P.
 XX
 PA (HYBR-) HYBRIGENICS.
 XX
 PI Legrain P;
 XX
 DR WPI; 2002-599706/64.
 DR N-PSDB; ABS51567.

XX
 PT New complex of protein-protein interactions between a bait Shigella
 PT flexneri polypeptide and a prey mammalian or human placenta polypeptide
 PT for treating or preventing bacillary dysentery in a mammal or human.
 XX
 PS Claim 7; Page 117-118; 162pp; English.

CC The invention relates to a complex of protein-protein interactions
 CC between a Shigella flexneri polypeptide (e.g. ospB, ospD, ipaD, ipaC,
 CC ipaH9.8, ospG and ospC1) and a mammalian polypeptide defined in the
 CC specification. The complexes are formed using the Yeast two-hybrid
 CC system. Also included are (1) a recombinant host cell expressing the
 CC polypeptide defined in the specification; (2) a recombinant host cell expressing the
 CC compound that inhibits or activates the polypeptide defined in the
 CC specification; (3) a modulating compound obtained from the method of (2); (4) a SID
 CC (selected interacting domain) polypeptide or its fragment or variant
 CC above polypeptides a vector comprising (5) a recombinant host cell
 CC containing the vector; and (10) a protein chip comprising Shigella
 CC polypeptide or polynucleotide is useful for treating or preventing the compound,
 CC shigellosis (bacillary dysentery) in a human or mammal. The present
 CC sequence represents a human prey protein isolated by the yeast two-hybrid
 XX assay, forming a complex of the invention with a shigella protein
 SQ

Query Match
 Best Local Similarity 45.6%; Score 900.5; DB 5; Length 418;
 Matches 178; Conservative 77; Mismatches 112; Indels 13; Gaps 5;

Qy 6 KVFKKCAPNKGKVTLQMGKRD**FVDHSGV**EPIDGIWVLD**DEYIRDNRKVFGQIVCSFRYGR** 65
 Db 7 RVF**KKASPN**GKLTIVLGKRDFV**DHIDLVD**PVGWVL**DPEYI**KE-RRVYV**TLCAFRYGR** 65
 Qy 66 E**DEEV**MG**LNFO**KELCL**A**SE**QIYPR**E**KSDKE**Q**TQ**ER**LKKLGSNAI**P**FEN**ISPNAPS 125
 Db 66 ED**DVLG**LT**FRKDLF**V**ANVQSF**PPAP**E**D**KKPL**TR**Q**ER**LKKLGE**H**EAYPFT**FEIPPNLPC 125
 Qy 126 S**T**VLQ**G**ED**DNGDPCGVSY**Y**KI**F**AGE**SET**DR**TH**RSTV**TL**GIRKIQ**FA**PTKQGQ**PC**T** 185
 Db 126 S**T**VLQ**G**ED**DNGDPCGVSY**Y**KI**F**AGE**SET**DR**TH**RSTV**TL**GIRKIQ**FA**PTKQGQ**PC**T** 185
 Qy 186 VRKDFM**LSPGE**LE**EV**TL**DQ**LY**LH**GER**I**G**N**IC**R**NS**N**K**M**V**K**K**I**AM**VQ**Q**G**VD**WV**I**FQ** 245
 Db 186 T**T**RF**QFLMSD**K**P**L**H**LE**A**SL**D**K**E**I**Y**H**G**EP**I**S**V**N**H**V**T**N**N**T**N**K**T**V**K**K**I**K**S**V**R**Q**A**D**I**C**L**F**N** 245
 Qy 246 T**AQYKCPV**ME**EADD**--**T**V**APS****S**T**FCKV**Y**T**TL**P**LAN**R**E**K**RG**LA**D**G**K**L**K**H**ED**T**N**L****A**S 305
 Db 306 T**L**LAQ**PDQ**D**RG**AV**GI**ST**A**Y**KV**K**L**F**L**--**G**AL**G**EL**S**A---**E**LP**FVLM**H**P**K**G**T**--**A 355
 Qy 356 KV**I**HAD**SQAD**VE**TR**Q**D**T**I**D 375
 Db 364 EV**PENETPV**D**TN**IEL**D**T**N**D 383

RESULT 12

ADQ89786
 ID ADQ89786 standard; protein; 418 AA.
 XX
 AC ADQ89786;
 DT 21-OCT-2004 (first entry)
 XX
 DE Antagonist of cell cycle progression polypeptide #108.

KW Cytostatic; cancer; cell division cycle; mitosis; meiosis;
 KW cell cycle progression.
 XX
 OS Homo sapiens.

XX
 PN WO20040653362-A2.
 XX
 PD 29-JUL-2004.
 XX
 PR 31-DEC-2003; 2003WO-GB005635.
 XX
 PR 06-MAY-2003; 2003US-0439123P.
 XX
 PA (CYCL-) CYCLACEL LTD.
 XX
 PI Glover D, Bell G, Frenz L, Midgley C;
 XX
 DR WPI; 2004-544089/52.
 XX
 DR N-PSDB; ADQ89785.

PT New cell cycle progression genes and proteins for modulating cell cycle
 PT progression in cells, for preventing, treating or diagnosing cell cycle
 PT proliferative diseases (e.g. cancer) or for identifying modulators of
 XX

PS Claim 2; SEQ ID NO 216; 461pp; English.

CC The present invention relates to a polynucleotide for preventing,
 CC treating or diagnosing a disease in an individual. The composition or the
 CC polypeptide, polynucleotide or RNA precursor, or antibody is useful for
 CC diagnosing, preventing or treating diseases (e.g. cell proliferative
 CC diseases such as cancer) in an individual. These may also be used for
 CC identifying the substances capable of binding to or modulating the function
 CC of the polypeptide, capable of affecting the function of the
 CC corresponding gene, or capable of inhibiting the cell division cycle or
 CC sequence represents an antagonist of cell cycle progression protein
 XX
 SQ Sequence 418 AA;

Query Match

Best Local Similarity 45.6%; Score 900.5; DB 8; Length 418;
 Matches 178; Conservative 77; Mismatches 112; Indels 13; Gaps 5;

Qy 6 KVFKKCAPNKGKVTLQMGKRD**FVDHSGV**EPIDGIWVLD**DEYIRDNRKVFGQIVCSFRYGR** 65
 Db 7 RVF**KKASPN**GKLTIVLGKRDFV**DHIDLVD**PVGWVL**DPEYI**KE-RRVYV**TLCAFRYGR** 65
 Qy 66 E**DEEV**MG**LNFO**KELCL**A**SE**QIYPR**E**KSDKE**Q**TQ**ER**LKKLGSNAI**P**FEN**ISPNAPS 125
 Db 66 ED**DVLG**LT**FRKDLF**V**ANVQSF**PPAP**E**D**KKPL**TR**Q**ER**LKKLGE**H**EAYPFT**FEIPPNLPC 125
 Qy 126 S**T**VLQ**G**ED**DNGDPCGVSY**Y**KI**F**AGE**SET**DR**TH**RSTV**TL**GIRKIQ**FA**PTKQGQ**PC**T** 185
 Db 126 S**T**VLQ**G**ED**DNGDPCGVSY**Y**KI**F**AGE**SET**DR**TH**RSTV**TL**GIRKIQ**FA**PTKQGQ**PC**T** 185
 Qy 186 VRKDFM**LSPGE**LE**EV**TL**DQ**LY**LH**GER**I**G**N**IC**R**NS**N**K**M**V**K**K**I**AM**VQ**Q**G**VD**WV**I**FQ** 245
 Db 186 T**T**RF**QFLMSD**K**P**L**H**LE**A**SL**D**K**E**I**Y**H**G**EP**I**S**V**N**H**V**T**N**N**T**N**K**T**V**K**K**I**K**S**V**R**Q**A**D**I**C**L**F**N** 245
 Qy 246 T**AQYKCPV**ME**EADD**--**T**V**APS****S**T**FCKV**Y**T**TL**P**LAN**R**E**K**RG**LA**D**G**K**L**K**H**ED**T**N**L****A**S 305
 Db 306 T**L**LAQ**PDQ**D**RG**AV**GI**ST**A**Y**KV**K**L**F**L**--**G**AL**G**EL**S**A---**E**LP**FVLM**H**P**K**G**T**--**A 355
 Qy 356 KV**I**HAD**SQAD**VE**TR**Q**D**T**I**D 375
 Db 364 EV**PENETPV**D**TN**IEL**D**T**N**D 383

CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
 CC patient did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 XX [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences)

SQ Sequence 369 AA;

Query Match
 Best Local Similarity 45.1%; Score 890; DB 4; Length 369;
 Matches 171; Conservative 75; Mismatches 100; Indels 6; Gaps 4;

QY 6 KVFKKCAPNGKVTLYMGKRDVFHDHSGVEPIDGIVWLDEYIRDNRKVFGQIVCSFRYGR 65
 Db 7 RVFKKASPNGKLTIVLGKRDVFHDHIDLVDPVGWVLVNDPEYLYKE-RRVYVTLCAFRYGR 65
 QY 66 EDEEVMLNFOKELCLASEQTYPRPEKSDKEOTKLOQERLKLQGKSNATPFENISPNA 125
 Db 66 EDLDVIGLTSFRKOLFVANVQSFPPAEDKKPLTRQERLIKIGEHAYPEFTFEPNLPC 125
 QY 126 SVTLQQGEDDNGDPPCGVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQOPCTL 185
 Db 126 SVTLQPGPDTGKACGVDYEAKAFCALNLEEKIHKRNSVGLVIRKVOAPERPGQOPTAE 185
 QY 186 VRKDFMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKMKVKKIKAMVQGVDFVLFQ 245
 Db 186 TTRQFLMSDKPLHLEASLDKEIYHGEPISVNVHVTNNNTKTEVKIKISVRQYADICLLEN 245
 QY 246 NGSYRNTVASLETSEGCPIOPGSSLQKVMYLTPLSSNKQRGIALDGQIKRQDQCLAST 305
 Db 246 TAQYKCPVAMEADD-TVAPSSTFCKVYLTTPFLANNREKRGGLADGKLUEDTNLASS 303
 QY 306 TLAQDQDRAFTGVIISYAVKVKLFLGALGELSAELPFLMHPK 355
 Db 304 TLLREGANREILGILIVSYKVKVQLVV-SRGGDVAVELPFTLMPKAQRGTPA 354

SQ Sequence 382 AA;

Query Match
 Best Local Similarity 48.3%; Score 885; DB 4; Length 382;
 Matches 167; Conservative 77; Mismatches 98; Indels 4; Gaps 3;

QY 6 KVFKKCAPNGKVTLYMGKRDVFHDHSGVEPIDGIVWLDEYIRDNRKVFGQIVCSFRYGR 65
 Db 8 RVFKKSSPNCKLTIVLGKRDVFHDHDKVDPVGWVLVDPDYLKD-RKVFTLTCAFRYGR 66
 QY 66 EDEEVMLNFOKELCLASEQTYPRPEKSDKEOTKLOQERLKLQGKSNATPFENISPNA 125
 Db 67 EDLDVIGLTSFRKOLFIAFYQAPPVNPFRPPTRLQDRLRLKGQHAPFFFTIPQNLPC 126
 QY 126 SVTLQQGEDDNGDPPCGVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQOPCTL 185
 Db 127 SVTLQPGPDTGKACGVDYEAKAFCALNLEEKIHKRNSVGLVIRKVOAPERPGQOPTAE 186
 QY 186 VRKDFMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKMKVKKIKAMVQGVDFVLFQ 245
 Db 187 TTRHFLMSDRSLHLEASLDKEIYHGEPISVNVHVTNNNTKTEVKIKISVRQYADICLLEN 304
 QY 246 NGSYRNTVASLETSEGCPIOPGSSLQKVMYLTPLSSNKQRGIALDGQIKRQDQCLAST 305
 Db 247 TAQYKCPVAMEADD-QVSPPSSTFCKVYLTTPFLANNREKRGGLADGKLUEDTNLASS 304
 QY 306 TLAQDQDRAFTGVIISYAVKVKLFLGALGELSAELPFLMHPK 351
 Db 305 TIVKEGANKEVILGILIVSYRVKVKLVV-SRGGDVAVELPFTLMPKAQRGTPA 349

SQ Sequence 369 AA;

XX PA (MILL-) MILLENNUM PHARM INC.
 XX PI Bernstein G;
 XX DR WPI; 2001-602637/68.

XX PT Identifying a G protein-coupled receptor ligand, useful for treating e.g. retinitis pigmentosa, color blindness or neurological disorders, uses phosphorylation-independent arrestin mutants particularly suited for in vitro screening assays.

XX PS Disclosure; Page 47; 47pp; English.

CC The present sequence represents an exemplary phosphorylation-independent arrestin mutant. Such mutants are used in screening assays to identify CC ligands and/or modulators of G protein-coupled receptors (GPCRs). A CC method for identifying a GPCR ligand comprises contacting a composition comprising the GPCR and a constitutively active arrestin mutant with a CC modulatory binding of arrestin to the GPCR, where modulation of CC used for identifying potential ligands is a GPCR ligand. The method is particularly modulators, for use as human therapeutics. Modulators of GPCRs, CC may be used for treating patients having e.g. retinitis pigmentosa, CC stationary night blindness, colour blindness, nephrogenic DI, isolated CC glucocorticoid deficiency, hyperfunctioning thyroid adenomas, familial CC hypocalciuric hypercalcemia, hyperparathyroidism and neurological CC disorders. The methods may be used for screening pluralities of test compounds (e.g. a small molecule library of compounds) or a composition containing a plurality of GPCRs. The methods may be used in screening CC assays for identification of natural and surrogate agonists of orphan GPCRs, and for identification of GPCR antagonists and/or agonists CC XX XX SQ Sequence 382 AA;

Query Match
 Best Local Similarity 48.3%; Score 885; DB 4; Length 382;
 Matches 167; Conservative 77; Mismatches 98; Indels 4; Gaps 3;

QY 6 KVFKKCAPNGKVTLYMGKRDVFHDHSGVEPIDGIVWLDEYIRDNRKVFGQIVCSFRYGR 65
 Db 8 RVFKKSSPNCKLTIVLGKRDVFHDHDKVDPVGWVLVDPDYLKD-RKVFTLTCAFRYGR 66
 QY 66 EDEEVMLNFOKELCLASEQTYPRPEKSDKEOTKLOQERLKLQGKSNATPFENISPNA 125
 Db 67 EDLDVIGLTSFRKOLFIAFYQAPPVNPFRPPTRLQDRLRLKGQHAPFFFTIPQNLPC 126
 QY 126 SVTLQQGEDDNGDPPCGVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQOPCTL 185
 Db 127 SVTLQPGPDTGKACGVDYEAKAFCALNLEEKIHKRNSVGLVIRKVOAPERPGQOPTAE 186
 QY 186 VRKDFMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKMKVKKIKAMVQGVDFVLFQ 245
 Db 187 TTRHFLMSDRSLHLEASLDKEIYHGEPISVNVHVTNNNTKTEVKIKISVRQYADICLLEN 304
 QY 246 NGSYRNTVASLETSEGCPIOPGSSLQKVMYLTPLSSNKQRGIALDGQIKRQDQCLAST 305
 Db 247 TAQYKCPVAMEADD-QVSPPSSTFCKVYLTTPFLANNREKRGGLADGKLUEDTNLASS 304
 QY 306 TLAQDQDRAFTGVIISYAVKVKLFLGALGELSAELPFLMHPK 351
 Db 305 TIVKEGANKEVILGILIVSYRVKVKLVV-SRGGDVAVELPFTLMPKAQRGTPA 349

Search completed: February 9, 2005, 23:42:08
 Job time : 167 secs

PD 13-SEPP-2001.
 XX 05-MAR-2001; 2001WO-US007304.
 XX PR 03-MAR-2000; 2000US-0186706P.

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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 9, 2005, 23:44:27 ; Search time 43 Seconds (without alignments)
 664.897 Million cell updates/sec

Perfect score: 1973
 Sequence: 1 MYVNFKVFKCAPPNGKVTLV.....ADVETFRQPTIDQASVDFE 383

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

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5: /cgn2_6/ptodata/1/iaa/6C_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULTS

RESULT 1
 US-09-880-137-3
 ; Sequence 3, Application US/09880137
 ; Patent No. 6640025

; GENERAL INFORMATION:

; APPLICANT: Bernstein, Gabriel

; TITLE OF INVENTION: METHODS OF ASSAYING FOR G PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS

; FILE REFERENCE: MNT-131

; CURRENT APPLICATION NUMBER: US/09/880,137

; CURRENT FILING DATE: 2001-03-05

; PRIOR APPLICATION NUMBER: US 60/186,706

; PRIOR FILING DATE: 2000-03-03

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 410

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-880-137-3

ALIGNMENTS

SEQUENCE ALIGNMENT

Query Match Description

Best Local Similarity 46.0%; Score 907.5; DB 4; Length 410;
 Matches 176; Conservative 78; Mismatches 112; Indels 7; Gaps 4;

QY 6 KVFKKCAPPNGKVTLVLYNGKRDVFHDVSGVVEPIDGIVWLDEYIRDNRKVFCQIVCSFRYGR 65
 Db 7 RVFKKASPNKGKLUVYLGKRDVFHDVLDPVGVVLVDPPEYKLRVVTLCAFRYGR 65

QY 66 EDEDEVMLNFOKELCLASEQIYPREKSDKEQTKLQERLLKKLGSNAIPFTNTSPNAPS 125
 Db 66 EDDVIGLTFRKDLFVANVOSFPPAPEDKKPLTRLQERLIKKGHEAYPFTEIPPNLPC 125

QY 126 SVTLQQGEDDNGDPCCGYSYVKIFAGESETDRTHRSTVTLGIRKTOEAPTKDQGQPC 185
 Db 126 SVTLQPGPBDTGKACGVDYEVKAFAENLEEKIHKRNSVRLVIRKQYAPERPGPQPTAE 185

QY 186 VRKDFMLISCGELELETVLKDOLYKLYGERIGVNICIRNNSNKVKKIKAMVQOGVVDVLFQ 245
 Db 186 TTRQFLMSDKPLHLEASLIDKEIYHGEPISVNVHVTNTNKTVKIKTSVRQYADICLFN 245

QY 246 NGSYRNTVASLETSEGCPIOPGSSLQVKMYLTPPLSSNKQRGQIALDQKIQKRDQCLAST 305
 Db 246 TAQYKCPVAMEADD-TVAPSSTFCKVYTLPEFLANNREKGGLAIDCKLKHEDTNLASS 303

QY 306 TLLAQDQDRAFTGIVISAVRKVLFLGALGGELSAELPFVLMKPGTK--AKVHADS 362
 Db 304 TLLREGANREILGILIVSYKVVKL-VESRGDDVAVELPFTLMHPKPKKEPPREVENET 362

QY 363 QADVETFRQPTID 375

```

Db      363 PVDTNLIELDTND 375
;
; SEQ ID NO 2
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-880-137-2

Query Match
Best Local Similarity 45.5%; Score 897.5; DB 4; Length 418;
Matches 178; Conservative 76; Mismatches 113; Indels 13; Gaps 5;
QY      6 KVFKKCAPNGKVLYMGRDFVDHVSGVEPIDGIVVLDEYIRDRNKRKFQGQIVCSFRYGR 65
Db      7 RVFKKASPNGLTVYLGKRDVFVDHIDLVDPGVVLVDPYLDK-RRVYVLTCAFRYGR 65
QY      66 EDEVMGLNFQKELCLASEQIYPRPEKSDEQTKLQERULLKKLGSNAIPFTNISPNA 125
Db      66 EDLDVGLTFRKDLFVNQSFPPAPEDKKPLTRLQERLIKKGHEHAYPFTFEIPPNLPC 125
QY      126 SVTLQOQGEDDNGDPCGVSYVKIFAGESETDRHRSVTGIRKQFAPTKQGQPC 125
Db      126 SVTLQOQGEDDNGDPCGVSYVKIFAGESETDRHRSVTGIRKQFAPTKQGQPC 125
QY      186 VRKDFMLSPGELELEVTLDKQLYLHGERIGVNICIRNNSNKVKIKAMVQGVDVLFQ 185
Db      186 TTRQFLMSDKPLHLEASLDKEIYHGEPISVNVHVTNTNKTVKKIKISVRQYADICLFN 245
QY      246 NGSYRNTVASLETSEGCPIQPGSSLQKWMYLTPLLSNKQRRGIALDGQIKRQDOCLAST 305
Db      246 TAQYKCPVAMEEADD--TVAPSSTFCKVYTLPFLANNREKRGALDGKLKHEDTNLASS 303
QY      306 TLLAQDQDRAFTGVILSYAVKVLF--1GALGGELSA----ELPFVLMMPKPGTK--A 355
Db      304 TLLRSGANREILGIVSVKVKVLUVESRGGLGDLASSDVAVELPFTMMPKKEEPPHR 363
QY      356 KVTHADSQADVETFRQDTID 375
Db      364 EVPENETPVDTNLIELDTND 383

RESULT 4
US-09-880-137-8
; Sequence 8, Application US/09880137
; Patent No. 6640025
; GENERAL INFORMATION:
; APPLICANT: Bernstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; FILE REFERENCE: MNI-131
; CURRENT APPLICATION NUMBER: US/09/880,137
; CURRENT FILING DATE: 2001-03-05
; PRIORITY FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Homo sapiens mutation
; OTHER INFORMATION: Description of Artificial Sequence: Homo sapiens mutation

Query Match
Best Local Similarity 44.9%; Score 885; DB 4; Length 382;
Matches 167; Conservative 77; Mismatches 98; Indels 4; Gaps 3;
QY      6 KVFKKCAPNGKVLYMGRDFVDHVSGVEPIDGIVVLDEYIRDRNKRKFQGQIVCSFRYGR 65
Db      8 RVFKKSSPNGLTVYLGKRDVFVDHLDKVDPGVVLVDPYLDK-RRVYVLTCAFRYGR 65
QY      66 EDEVMGLNFQKELCLASEQIYPRPEKSDEQTKLQERULLKKLGSNAIPFTNISPNA 125
Db      67 EDLDVGLTFRKDLFVNQSFPPAPEDKKPLTRLQERLIKKGHEHAYPFTFEIPPNLPC 126

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QY 126 SVTLOQGEDDNGDPGCVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGOQPCCTL 185
Db 127 SVTLOQGPEDTGKACGVDFEIRAFCAKSLEEKSHKRNSVRLVKQFAPEKPGPQPSAE 186
QY 186 VRKDFMLSPGELELEVTLDKOLYLYHGERIGVNICIRNNSNKMKIKAMVQOGVDFVLFO 245
Db 187 TTRHFLMSDRSLHLEASLDKELYHGEPLNVNVHVTNNSTKTVKKIVSVRQYADICLFS 246
QY 246 NGSYRNTVASLETSECGCPIOPGSSLQKVMYLTPLLSSNKQRGIALDQIKRQDOCLAST 305
Db 247 TAQYKCPVAQLEQDD-QVSPSSTFCVKVYTITPLLSDNREKRGGLADGKLKHEDTNLASS 304
QY 305 TIVKEGANKEVLGILVSYRVKVKLVV-SRGDDSVELPFVLMHPKP 349
Db 306 TLLAQPDQDARGVIIISYAVKVKLFLGALGGELSAELPFVLMHPKP 351
QY 306 TLLAQPDQDARGVIIISYAVKVKLFLGALGGELSAELPFVLMHPKP 351
Db 305 TIVKEGANKEVLGILVSYRVKVKLVV-SRGDDSVELPFVLMHPKP 349

RESULT 5
US-09-880-137-4
; sequence 4, Application US/09880137
; Patent No. 6640025
; GENERAL INFORMATION:
; APPLICANT: Bernstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
; FILE REFERENCE: MNI-131
; CURRENT APPLICATION NUMBER: US/09/880,137
; CURRENT FILING DATE: 2001-03-05
; PRIORITY APPLICATION NUMBER: US 60/186,706
; PRIORITY FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Homo sapiens mutation
; US-09-880-137-4

Query Match 44.6%; Score 880; DB 4; Length 409;
Best Local Similarity 48.0%; Pred. No. 2.2e-84;
Matches 166; Conservative 77; Mismatches 99; Indels 4; Gaps 3;
Matches 167; Conservative 77; Mismatches 98; Indels 4; Gaps 3;

QY 6 KVFKKCANGKVLYMGRDFDVFHSGVERPIGIVWLDDPEYIRDNRKVFQIVCSFRYGR 65
Db 8 RVFKKSSPNCKLTWYLGKRDVFVHLDKVDPDVGLVLPDPYLD-RKVFTLTCAFTRYGR 66
QY 126 SVTLOQGEDDNGDPGCVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGOQPCCTL 185
Db 127 SVTLOQGPEDTGKACGVDFEIRAFCAKSLEEKSHKRNSVRLVKQFAPEKPGPQPSAE 186
QY 186 VRKDFMLSPGELELEVTLDKOLYLYHGERIGVNICIRNNSNKMKIKAMVQOGVDFVLFO 245
Db 187 TTRHFLMSDRSLHLEASLDKELYHGEPLNVNVHVTNNSTKTVKKIVSVRQYADICLFS 246
QY 246 NGSYRNTVASLETSECGCPIOPGSSLQKVMYLTPLLSSNKQRGIALDQIKRQDOCLAST 305
Db 247 TAQYKCPVAQLEQDD-QVSPSSTFCVKVYTITPLLSDNREKRGGLADGKLKHEDTNLASS 304
QY 306 TLLAQPDQDARGVIIISYAVKVKLFLGALGGELSAELPFVLMHPKP 351
Db 305 TIVKEGANKEVLGILVSYRVKVKLVV-SRGDDSVELPFVLMHPKP 349

RESULT 6
US-09-880-137-7
; sequence 7, Application US/09880137
; Patent No. 6640025
; GENERAL INFORMATION:

Query Match 43.3%; Score 853.5; DB 4; Length 401;
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-8383

Best Local Similarity 46.1%; Pred. No. 1.4e-81; Matches 170; Conservative 75; Mismatches 111; Indels 13; Gaps 5; Qy 17 VTLVYMGKRDVFVDHVSGVVERIDGIWLDDEVIRDNRKVFGQIVCSFRYGREREDEVMLNFO 76 Db 1 LTVVYLGKRDVFVDHIDLVDVPGVVLVDPPEYLKE-RRVYVLTCAFRYGRERDLDVGLTFR 59 Qy 77 KELCLASEQIYPRPEKSDKEQTKLQERLLKKLGNSNAIPFTFNISPAPSSVTQGEDDN 136 Db 60 KOLFVANVOSFPPEKSDKEQTKLQERLLKKLGNSNAIPFTFNISPAPSSVTQGEDDN 136 Qy 137 GDPCCGVSYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQOPCTLVKDFMLSPGE 196 Db 120 GRACGVYDIEVKFCAENJEEKIKRNSVRVLVIRKVQYAPERPGPQPTAETTROFLMSDKP 179 Qy 197 LELEVTLDKOLYLGERICGNICIRNNSNKMKVKKIKAMVQOQGVQDVVLFONGSYRNTVDSL 256 Db 180 LHLEASLDKETIYVHGEPISVNVHVTNNNTKTVKKIKISVRQYADICLFTAQYKCPVAME 256 Qy 257 ETSEGCPIQPGSSLOKVMYLTPLLSSNKKQRGIALDQIKRQDQCLASTTLLAQPDORDA 316 Db 240 EADD--TVAPSSTFCKVYTTLTFLANNREKRGGLALDGKLKHEDTNLASSTLREGANREI 297 Qy 317 FGVIISYAVVKLFL--GALGGELSA---ELPFVLMHPKPGTK---AKVIHADSDQADV 366 Db 298 LGIIVSYVKVKLVSRGGGLGLASSDVAELPFTLMHPKKEEPHREVPENETPVDT 357 Qy 367 ETFRQDTID 375 Db 358 NLIELDTND 366

RESULT 8

US-09-949-016-8384
; Sequence 8384, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US/09/949, 016
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-949-016-8384

Query Match Best Local Similarity 43.3%; Score 853.5; DB 4; Length 401; Matches 170; Conservative 75; Mismatches 111; Indels 13; Gaps 5; Qy 17 VTLVYMGKRDVFVDHVSGVVERIDGIWLDDEVIRDNRKVFGQIVCSFRYGREREDEVMLNFO 76 Db 1 LTVVYLGKRDVFVDHIDLVDVPGVVLVDPPEYLKE-RRVYVLTCAFRYGRERDLDVGLTFR 59 Qy 77 KELCLASEQIYPRPEKSDKEQTKLQERLLKKLGNSNAIPFTFNISPAPSSVTQGEDDN 136 Db 60 KDLFVANVOSFPPEKSDKEQTKLQERLLKKLGNSNAIPFTFNISPAPSSVTQGEDDN 136 Qy 137 GDPCCGVSYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQOPCTLVKDFMLSPGE 196 Db 120 GRACGVYDIEVKFCAENJEEKIKRNSVRVLVIRKVQYAPERPGPQPTAETTROFLMSDKP 179

RESULT 9

US-09-880-137-6
; Sequence 6, Application US/09880137
; Patent No. 6640025
; GENERAL INFORMATION:
; APPLICANT: Bernstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; FILE REFERENCE: MNT-131
; CURRENT APPLICATION NUMBER: US/09/880, 137
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186, 706
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-137-6

Query Match Best Local Similarity 39.6%; Score 780.5; DB 4; Length 388; Matches 166; Conservative 79; Mismatches 125; Indels 19; Gaps 7; Qy 6 KVFKKCACPNGKVTLYMGKRDVFVDHVSGVVERIDGIWLDDEVIRDNRKVFGQIVCSFRYGR 65 Db 3 KVFKKTSNSNGKLSIYLGKRDVFVDHVDTVEPDIQVVLVDPPEYLKE-RCKLFVMLTCAFYGR 61 Qy 66 EDEDEVMLNFOKECLASEQIYPRPEKSDK-BQTKLQERLLKKLGNSNAIPFTFNISPAP 124 Db 62 DDLEVIGLTFRKDLVYQVTLQVVAEASSSPQGALTQVLRILHKGDNAYPFTLQMVNL 121 Qy 125 SSVTQGEDDNGDPCGVSYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQOPCT 184 Db 122 CSVTLQPGPEDAGKPGIDEEVKSFCAENPEETVSKRDVRLVVRKVQFAPPEAGPGPSA 181 Qy 185 LVRKDFMLSPGELELEVTLDKOLYLGERICGNICIRNNSNKMKVKKIKAMVQOQGVQDVVL 244 Db 182 QTIRRFLLSAQPLQLOAQMWDREVHYHGEPISVNVNSINCTNKVVKIKISVQDITDVLV 241 Qy 245 QNGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLLSSNKKQRGIALDQIKRQDQCLAS 304 Db 242 SLDKVTKTIVFQEFTE-TVAANSSFSQFASVTPILLASCKRGGLALDGKLKHEDTNLAS 299 Qy 305 TLLAQPDQDRAFTYVLTCAFRYGRERDLDVGLTFR 59 Qy 300 STIRPGMDKELIGLIVSYVKVRLVNLMSCCGILGDLTASDVGVELPVLVLPKHSHEA- 357 Db 358 THADSDQADV--ETFRQDTIDQASVDFE 383 Db 359 ---SSEDIVIEEFTRKGEESQKAVEAE 383

RESULT 10

US-09-880-137-5

; Sequence 5, Application US/09880137
; Patent No. 6640025
; GENERAL INFORMATION:
; APPLICANT: Bernstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; FILE REFERENCE: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
; CURRENT APPLICATION NUMBER: US/09/880,137
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-880-137-5

Query Match 38.9%; Score 767.5; DB 4; Length 315;
Best Local Similarity 48.0%; Pred. No. 1.2e-72; Gaps 2;
Matches 145; Conservative 66; Mismatches 88; Indels 3; Gaps 2;

Qy 6 KVFKKCAPNGKVTLYMGKRDFFDVHSGVVERIDGIVVLDDEYIRDNRKVFGQIVCSFRYGR 65
Db 8 RVFKKSSPNCKLTVLGKRDFFDVHLDKVDVDPGVVLVDPYLDK-RKVFTILTCAFRYGR 66

Qy 66 EEDEVWGLNFOKECLASERQYPRPEKSDKEQTKLQERLKKLGNSAIPFTENISPNAAPS 125
Db 67 EDLVLGLSFRKDLFIATYQAFFPVNPVPRPPTRLQDLRLKLGQAHPPFFRIPQNLPC 126

Qy 126 SVTLQOQEDDNGDPGCVSYVVKIFAGESETDRTRRSTVTLGIRKIQFAPTKOGQQPCTL 185
Db 127 SVTLQPGPDTGKACGGDFIRACAKSLEEKSHKRNSVRLVIRKQFAPKEKPGPQPSAE 186

Qy 186 VRKKDFMLSPGELELEVTLDKOLYLHGERIGVNICIRNNNSNKVKKIKAMVQOGVDVVLFO 245
Db 187 TTRHFLMSDRSLHLEASLDKELYVHGEPLNVNVHVTNNSTKTVKKIKVSVRQYADICLFS 246

Qy 246 NGSYRNTVASLETSEGCPIOPGSSLQKVMYLTPLISSNKORRGIALDGQIKRQDQCLAST 305
Db 247 TAQKCPVQAQLEDD-QVSPPSSTRCKVYTITPLSDNREKRGALDGKLIKEDTNLASS 304

Qy 306 TL 307
Db 305 TM 306

RESULT 12
US-09-270-767-58832
; Sequence 58832, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58832
; LENGTH: 197
; TYPE: PRT
; ORGANISM: *Drosophila melanogaster*
; US-09-270-767-58832

Query Match 16.0%; Score 316; DB 4; Length 197;
Best Local Similarity 49.6%; Pred. No. 4.3e-25; Gaps 1;
Matches 59; Conservative 25; Mismatches 33; Indels 2; Gaps 1;

Qy 235 VQGVGVVLFQNGSYRNTVASLETSEGCPIOPGSSLQKVMYLTPLISSNKORRGIALDGQ 294
Db 2 VRQFADICLFLSTAQKSVWAEIESEDGCQVAPGFTLSKVFELCPLLANNKDKWGLALDGQ 61

Qy 295 IKRQDQCLASTLLAOPDORDAFGVIIISYAVKVFLGA--LGGELSAELPFLVLMHPKP 351
Db 62 LKHEDTNLASSTLITNPQRESLIGIMHYKVVKLISSPLINGDLVAELPFTIMHPKP 120

RESULT 13
US-09-270-767-43475
; Sequence 43475, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767

NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9940
; LENGTH: 315

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; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43475
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: US-09-270-767-43475. Xaa means any amino acid

Query Match
Best Local Similarity 16.0%; Score 316; DB 4; Length 475;
Matches 59; Conservative 25; Mismatches 33; Indels 2; Gaps 1;
Qy 235 VQQGVDVVLFQONGSYRNTVASLETSEGCPIQPGSSLOKWMVLTPLSSNKORRGIAALPGQ 294
Db 280 VRQFADICLFLSTAQYKSVVAEIESEDGCQVARGFETSKVFEICPILANNKDKWGLALDGQ 339
Qy 295 IKRQDQCLASTTLAQPDQDRAFTYAVKVKLFLGA--LGGELSAELPFLVLMHPKP 351
Db 340 LKHEDTNLASSTLITNPAQRESIGIMWYKVKVKKLISPLLINGDLVAELPFTLMHPKP 398
RESULT 14
US-09-270-767-32381
; Sequence 32381, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and Proteins of Drosophila melanogaster
; FILE REFERENCE: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; NUMBER OF SEQ ID NOS: 1999-03-17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32381
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-32381

Query Match
Best Local Similarity 11.4%; Score 225; DB 4; Length 137;
Matches 52; Conservative 26; Mismatches 38; Indels 6; Gaps 4;
Qy 6 KVFKKCAPNGKVTLYMGKRDVFVHDHVGVEP--IDGIVVLDEYIRDNRKVFGQIVCSFRY 63
Db 19 RVKKRSPNVCVITYLPFREIT--LTGNNPSVLRGIVYDPKAIQGYR-WYAQLTITFRY 75
Qy 64 GREDEEVGLNPKQELCLASEQIYPRPEKSDEQ-TKLOERLKKLGSNAIPFTFNISP 122
Db 76 GREDEEVGLRFCNEAIMSLHQIWPRLLEPTPESSPLSQEALMKRIGDGAHPPFTLS 135
Qy 123 AP 124
Db 136 AP 137

Search completed: February 9, 2005, 23:55:39
Job time: 45 secs

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Om protein - protein search, using sw mode1

Run on: February 9, 2005, 23:23:01 ; Search time 130 Seconds
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Title: US-10-056-405-2
Perfect score: 1973
Sequence: 1 MVYNFKVFKKCAPNGKVTLY.....ADVETFRQDTIDQASVDFE 383
Scoring table: BLOSUM62
Searched: Gapop 10.0 , Gapext 0.5
Total number of hits satisfying chosen parameters: 1373511
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1973	100.0	383	US-10-094-240-2
2	1973	100.0	383	Sequence 2, Appli
3	1023	51.8	398	Sequence 2, Appli
4	982.5	49.8	401	Sequence 25, Appli
5	907.5	46.0	410	Sequence 27, Appli
6	907.5	46.0	410	Sequence 3, Appli
7	903.5	45.8	418	Sequence 3, Appli
8	903.5	45.8	418	Sequence 1, Appli
9	903.5	45.8	452	Sequence 1, Appli
10	900.5	45.6	418	Sequence 52, Appli
11	897.5	45.5	418	Sequence 52, Appli
12	897.5	45.5	418	Sequence 2, Appli
13	885	44.9	382	Sequence 2, Appli

US-10-094-240-2

Query Match Score 1973; DB 14; Length 383;
Best Local Similarity 100.0%; Pred. No. 4.4e-176;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVYNFKVFKKCAPNGKVTLY.....ADVETFRQDTIDQASVDFE 60
Db 1 MVYNFKVFKKCAPNGKVTLY.....ADVETFRQDTIDQASVDFE 60

Qy 61 FRYGREEDEVMGINFOKELCLASEQIYPRPEKSDKEQTKLQERLKKLGNSNAIPFTENIS 120
Db 61 FRYGREEDEVMGINFOKELCLASEQIYPRPEKSDKEQTKLQERLKKLGNSNAIPFTENIS 120

Qy 121 PNAPSSVTLQGEDDNGDPGVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQ 180
|||

Db 121 PNAPSSVTLQOGEDDNGDPGCVSYVKFAGESETDRTHRSTVTLGIRKIQFAPTKQGQ 180

Qy 181 QPCTLVRKDMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKVKIKAMVQQGV 240

Db 181 QPCTLVRKDMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKVKIKAMVQQGV 240

Qy 241 VVLFQNGSYRNTVASLETSEGCPRIQPGSSLQKVMYLTPLLSNKQRGIALDGQIKRQD 240

Db 241 VVLFQNGSYRNTVASLETSEGCPRIQPGSSLQKVMYLTPLLSNKQRGIALDGQIKRQD 240

Qy 301 CLASTTLLAQPDQDRAFTGVLISYAVKVKLFLGALGGESELPEVLMHPKPGTAKVHA 360

Db 301 CLASTTLLAQPDQDRAFTGVLISYAVKVKLFLGALGGESELPEVLMHPKPGTAKVHA 360

Qy 361 DSQADVETFROTDIDQOASVDFE 383

Db 361 DSQADVETFROTDIDQOASVDFE 383

RESULT 2
US-10-056-405-2

; Sequence 2, Application US/10056405

; GENERAL INFORMATION:
; APPLICANT: ZWIEBEL, LAURENCE J.

; TITLE OF INVENTION: MOSQUITO OLFACTORY GENES, POLYPEPTIDES, AND METHODS OF
; FILE REFERENCE: USE THEREOF

; CURRENT APPLICATION NUMBER: US/10/056,405

; PRIOR APPLICATION NUMBER: 2002-01-24

; NUMBER OF SEQ ID NOS: 25

; LENGTH: 398

; TYPE: PRT

; ORGANISM: Anopheles gambiae

US-10-056-405-2

Query Match

Best Local Similarity 100.0%; Score 1973; DB 14; Length 383;

Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVYNFKVKKKCAPNGKVTLYMGKRDVFVHDVSGVEPIDGIVVLDDEYIRDNRKVFGQIVCS 60

Db 1 MVVAVKVKSAENGKLTWVLGKDFIDHTOYCDPIDS 60

Qy 61 FRYGREDDEVWGLNFOKELCASEQYPRPEKSDEQTKLQERLKLKGNSNAPFTENIS 59

Db 60 YRYGREDDEVWGLVFKSKENVLTKEQIYPM-ENANMEMTPM0ERLYKUGANAPFTFHFP 118

Qy 121 PNAPSSVTLQOGEDDNGDPGCVSYVKFAGESETDRTHRSTVTLGIRKIQFAPTKQGQ 180

Db 121 PNAPSSVTLQOGEDDNGDPGCVSYVKFAGESETDRTHRSTVTLGIRKIQFAPTKQGQ 180

Qy 181 Q-PCTLVRKDMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKVKIKAMVQQGV 239

Db 181 Q-PCTLVRKDMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKVKIKAMVQQGV 239

Qy 239 EVTMV-NAQFSKHKIASLETREGCTPFGASFTKSFLVPLASSNKDRRGIALDGQIKRQD 297

Db 239 EVTMV-NAQFSKHKIASLETREGCTPFGASFTKSFLVPLASSNKDRRGIALDGQIKRQD 297

Qy 300 QCLASTTLLAQPD-ORDAFGVLISYAVKVKLFLGALGGESELPEVLMHPKPGTAKVHA 360

Db 300 QCLASTTLLAQPD-ORDAFGVLISYAVKVKLFLGALGGESELPEVLMHPKPGTAKVHA 360

Qy 357 VHADSOADVETFROTDIDQOASVDFE 383

Db 357 VHADSOADVETFROTDIDQOASVDFE 383

Qy 383 VHADSOADVETFROTDIDQOASVDFE 383

RESULT 4
US-10-094-240-27

; Sequence 27, Application US/10094240

; GENERAL INFORMATION:
; APPLICANT: ZWIEBEL, LAURENCE J.

; TITLE OF INVENTION: ARRESTIN GENE, POLYPEPTIDE, AND METHODS OF USE THEREOF

; FILE REFERENCE: N8289

; CURRENT APPLICATION NUMBER: US/10/094,240

; PRIOR APPLICATION NUMBER: 2001-03-08

; PRIOR FILING DATE: 2002-01-24

; NUMBER OF SEQ ID NOS: 60/264,649

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 27

; LENGTH: 401

;

TYPE: PRT

ORGANISM: Drosophila melanogaster

US-10-094-240-27

Query Match 49.8%; Score 982.5; DB 14; Length 401;

Best Local Similarity 48.7%; Pred. No. 3.3e-83; Mismatches 115; Indels 13; Gaps 6;

Matches 191; Conservative 73; Mismatches 115; Indels 13; Gaps 6;

;

Qy 1 MVYNPKVFKKCAPNGKVTLYMGKRDFFDHFVSGVEPIDGIVVLDEYIRDNRKVFQGIVCSFRYGR 60

Db 1 MVVSVKVKKATPNKGKTFYLRHIDYCDPVGIVVEPDYLK-NRKVFGOLATT 59

Qy 61 FRYGREEDEVMGLNFQKELCILASEQIYPRPEKSDEQTKLQERLLKKIGGSNAIPFTFNISPNAPS 120

Db 60 YRYGEEDEVMGKFKESKELLICLREQIVPM-TNPNMENTPMQEKLVKUJGSNAIPFTFNIS 118

Qy 121 PNAPSSVTLQQGEDDNGDPGVSYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQ 180

Db 119 PNSPSSVTLQQGEDDNGKPGVEYTAFVGDSEDRQHKRSMSVLVIKKQYAPLNRCQ 178

Qy 181 Q-PTCLVLRKDFMLSPGELELEVTLDKQLYLHGERIGVNICIRNNNSNKVKIKAMVQGV 239

Db 179 RLPSLVLVKGFTFSNGKISLEVTLDREIYVHGEKTAATVQVSNNSKVKIKCFIVQHT 238

Qy 240 DVVLPLQNGSYRNTVASLETSEGCPIQPGSSLQKVMYLPLSSNKQRGIALDQIKRQD 299

Db 239 EITMV-NAQFSKHKVAQLETKEGCPIRPGANLTKTFYLIPLAANNKDRHGLADGHILKED 297

Qy 300 QCLASTTLLAQ-PDQRDAFGVIIISYAVKVKLFLGALGGELSAELPFLMHPKPGT--- 353

Db 298 VNLLASSTMVQEGKSTGDACTGIVIVSIVRIKLNCGTLLGEMOTDVFKLQOPAPGTLIEKCR 357

Qy 354 ---KAKVHADSDQADVETFRQDTIDQASVDF 382

Db 358 SNAMEKKMSIEQHNVKGYYQDDDDNIVFEDF 389

;

RESULT 5

US-09-880-137-3

;

Sequence 3, Application US/09880137

;

Patent No. US20020031295A1

;

GENERAL INFORMATION:

;

APPLICANT: Bernstein, Gabriel

;

TITLE OF INVENTION: METHODS OF ASSAYING FOR G PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS

;

FILE REFERENCE: MNI-131

;

CURRENT APPLICATION NUMBER: US/09/800,137A

;

CURRENT FILING DATE: 2001-03-05

;

PRIOR APPLICATION NUMBER: US 60/186,706

;

PRIOR FILING DATE: 2000-03-03

;

NUMBER OF SEQ ID NOS: 8

;

SOFTWARE: FastSEQ for Windows Version 4.0

;

SEQ ID NO 3

;

LENGTH: 410

;

TYPE: PRT

;

ORGANISM: Homo sapiens

;

US-09-800-137A-3

;

Query Match 46.0%; Score 907.5; DB 10; Length 410;

Best Local Similarity 47.2%; Pred. No. 3.7e-76; Mismatches 112; Indels 7; Gaps 4;

Matches 176; Conservative 78; Mismatches 112; Indels 7; Gaps 4;

;

Qy 6 KVFKKCAPNGKVTLYMGKRDFFDHFVSGVEPIDGIVVLDEYIRDNRKVFQGIVCSFRYGR 65

Db 7 RVFKKASPNKGKTFYLRHIDYCDPVGIVVEPDYLK-NRKVFGOLATT 65

Qy 66 EEDEVMLNFOKELCILASEQIYPRPEKSDEQTKLQERLLKKIGGSNAIPFTFNISPNAPS 125

Db 66 EDLVLGLTRFKDVLVANVQSFPPAPEDKKPLTRIQLQERLIKULGEHAYPFTFEIPPNLPC 125

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NUMBER OF SEQ ID NOS: 8

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SOFTWARE: FastSEQ for Windows Version 4.0

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SEQ ID NO 3

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LENGTH: 410

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TYPE: PRT

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ORGANISM: Homo sapiens

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US-09-880-137-3

;

Query Match 46.0%; Score 907.5; DB 9; Length 410;

Best Local Similarity 47.2%; Pred. No. 3.7e-76; Mismatches 112; Indels 7; Gaps 4;

Matches 176; Conservative 78; Mismatches 112; Indels 7; Gaps 4;

;

Qy 6 KVFKKCAPNGKVTLYMGKRDFFDHFVSGVEPIDGIVVLDEYIRDNRKVFQGIVCSFRYGR 65

Db 7 RVFKKASPNKGKTFYLRHIDYCDPVGIVVEPDYLK-NRKVFGOLATT 65

Qy 66 EEDEVMLNFOKELCILASEQIYPRPEKSDEQTKLQERLLKKIGGSNAIPFTFNISPNAPS 125

Db 66 EDLVLGLTRFKDVLVANVQSFPPAPEDKKPLTRIQLQERLIKULGEHAYPFTFEIPPNLPC 125

;

NUMBER OF SEQ ID NOS: 8

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SOFTWARE: FastSEQ for Windows Version 4.0

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SEQ ID NO 3

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LENGTH: 410

;

TYPE: PRT

;

ORGANISM: Homo sapiens

;

US-09-880-137A-3

;

Query Match 46.0%; Score 907.5; DB 9; Length 410;

Best Local Similarity 47.2%; Pred. No. 3.7e-76; Mismatches 112; Indels 7; Gaps 4;

Matches 176; Conservative 78; Mismatches 112; Indels 7; Gaps 4;

;

Qy 6 KVFKKCAPNGKVTLYMGKRDFFDHFVSGVEPIDGIVVLDEYIRDNRKVFQGIVCSFRYGR 65

Db 7 RVFKKASPNKGKTFYLRHIDYCDPVGIVVEPDYLK-NRKVFGOLATT 65

Qy 66 EEDEVMLNFOKELCILASEQIYPRPEKSDEQTKLQERLLKKIGGSNAIPFTFNISPNAPS 125

Db 66 EDLVLGLTRFKDVLVANVQSFPPAPEDKKPLTRIQLQERLIKULGEHAYPFTFEIPPNLPC 125

;

NUMBER OF SEQ ID NOS: 8

;

SOFTWARE: FastSEQ for Windows Version 4.0

;

SEQ ID NO 3

;

LENGTH: 410

;

TYPE: PRT

;

ORGANISM: Homo sapiens

;

US-09-880-137-3

;

Query Match 46.0%; Score 907.5; DB 9; Length 410;

Best Local Similarity 47.2%; Pred. No. 3.7e-76; Mismatches 112; Indels 7; Gaps 4;

Matches 176; Conservative 78; Mismatches 112; Indels 7; Gaps 4;

;

Qy 6 KVFKKCAPNGKVTLYMGKRDFFDHFVSGVEPIDGIVVLDEYIRDNRKVFQGIVCSFRYGR 65

Db 7 RVFKKASPNKGKTFYLRHIDYCDPVGIVVEPDYLK-NRKVFGOLATT 65

Qy 66 EEDEVMLNFOKELCILASEQIYPRPEKSDEQTKLQERLLKKIGGSNAIPFTFNISPNAPS 125

Db 66 EDLVLGLTRFKDVLVANVQSFPPAPEDKKPLTRIQLQERLIKULGEHAYPFTFEIPPNLPC 125

;

NUMBER OF SEQ ID NOS: 8

;

SOFTWARE: FastSEQ for Windows Version 4.0

;

SEQ ID NO 3

;

LENGTH: 410

;

TYPE: PRT

;

ORGANISM: Homo sapiens

;

US-09-880-137-3

;

Query Match 46.0%; Score 907.5; DB 9; Length 410;

Best Local Similarity 47.2%; Pred. No. 3.7e-76; Mismatches 112; Indels 7; Gaps 4;

Matches 176; Conservative 78; Mismatches 112; Indels 7; Gaps 4;

;

Qy 6 KVFKKCAPNGKVTLYMGKRDFFDHFVSGVEPIDGIVVLDEYIRDNRKVFQGIVCSFRYGR 65

Db 7 RVFKKASPNKGKTFYLRHIDYCDPVGIVVEPDYLK-NRKVFGOLATT 65

Qy 66 EEDEVMLNFOKELCILASEQIYPRPEKSDEQTKLQERLLKKIGGSNAIPFTFNISPNAPS 125

Db 66 EDLVLGLTRFKDVLVANVQSFPPAPEDKKPLTRIQLQERLIKULGEHAYPFTFEIPPNLPC 125

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NUMBER OF SEQ ID NOS: 8

;

SOFTWARE: FastSEQ for Windows Version 4.0

;

SEQ ID NO 3

;

LENGTH: 410

;

TYPE: PRT

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ORGANISM: Homo sapiens

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US-09-880-137-3

;

Query Match 46.0%; Score 907.5; DB 9; Length 410;

Best Local Similarity 47.2%; Pred. No. 3.7e-76; Mismatches 112; Indels 7; Gaps 4;

Matches 176; Conservative 78; Mismatches 112; Indels 7; Gaps 4;

;

Qy 6 KVFKKCAPNGKVTLYMGKRDFFDHFVSGVEPIDGIVVLDEYIRDNRKVFQGIVCSFRYGR 65

Db 7 RVFKKASPNKGKTFYLRHIDYCDPVGIVVEPDYLK-NRKVFGOLATT 65

Qy 66 EEDEVMLNFOKELCILASEQIYPRPEKSDEQTKLQERLLKKIGGSNAIPFTFNISPNAPS 125

Db 66 EDLVLGLTRFKDVLVANVQSFPPAPEDKKPLTRIQLQERLIKULGEHAYPFTFEIPPNLPC 125

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NUMBER OF SEQ ID NOS: 8

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SOFTWARE: FastSEQ for Windows Version 4.0

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SEQ ID NO 3

;

LENGTH: 410

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TYPE: PRT

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ORGANISM: Homo sapiens

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US-09-880-137-3

;

Query Match 46.0%; Score 907.5; DB 9; Length 410;

Best Local Similarity 47.2%; Pred. No. 3.7e-76; Mismatches 112; Indels 7; Gaps 4;

Matches 176; Conservative 78; Mismatches 112; Indels 7; Gaps 4;

;

Qy 6 KVFKKCAPNGKVTLYMGKRDFFDHFVSGVEPIDGIVVLDEYIRDNRKVFQGIVCSFRYGR 65

Db 7 RVFKKASPNKGKTFYLRHIDYCDPVGIVVEPDYLK-NRKVFGOLATT 65

Qy 66 EEDEVMLNFOKELCILASEQIYPRPEKSDEQTKLQERLLKKIGGSNAIPFTFNISPNAPS 125

Db 66 EDLVLGLTRFKDVLVANVQSFPPAPEDKKPLTRIQLQERLIKULGEHAYPFTFEIPPNLPC 125

;

NUMBER OF SEQ ID NOS: 8

;

SOFTWARE: FastSEQ for Windows Version 4.0

;

SEQ ID NO 3

;

LENGTH: 410

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TYPE: PRT

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ORGANISM: Homo sapiens

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US-09-880-137-3

;

Query Match 46.0%; Score 907.5; DB 9; Length 410;

Best Local Similarity 47.2%; Pred. No. 3.7e-76; Mismatches 112; Indels 7; Gaps 4;

Matches 176; Conservative 78; Mismatches 112; Indels 7; Gaps 4;

;

Qy 6 KVFKKCAPNGKVTLYMGKRDFFDHFVSGVEPIDGIVVLDEYIRDNRKVFQGIVCSFRYGR 65

Db 7 RVFKKASPNKGKTFYLRHIDYCDPVGIVVEPDYLK-NRKVFGOLATT 65

Qy 66 EEDEVMLNFOKELCILASEQIYPRPEKSDEQTKLQERLLKKIGGSNAIPFTFNISPNAPS 125

Db 66 EDLVLGLTRFKDVLVANVQSFPPAPEDKKPLTRIQLQERLIKULGEHAYPFTFEIPPNLPC 125

;

NUMBER OF SEQ ID NOS: 8

;

SOFTWARE: FastSEQ for Windows Version 4.0

;

SEQ ID NO 3

;

LENGTH: 410

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TYPE: PRT

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ORGANISM: Homo sapiens

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US-09-880-137-3

;

Query Match 46.0%; Score 907.5; DB 9; Length 410;

Best Local Similarity 47.2%; Pred. No. 3.7e-76; Mismatches 112; Indels 7; Gaps 4;

Matches 176; Conservative 78; Mismatches 112; Indels 7; Gaps 4;

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Qy 6 KVFKKCAPNGKVTLYMGKRDFFDHFVSGVEPIDGIVVLDEYIRDNRKVFQGIVCSFRYGR 65

Db 7 RVFKKASPNKGKTFYLRHIDYCDPVGIVVEPDYLK-NRKVFGOLATT 65

Qy 66 EEDEVMLNFOKELCILASEQIYPRPEKSDEQTKLQERLLKKIGGSNAIPFTFNISPNAPS 125

Db 66 EDLVLGLTRFKDVLVANVQSFPPAPEDKKPLTRIQLQERLIKULGEHAYPFTFEIPPNLPC 125

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NUMBER OF SEQ ID NOS: 8

;

SOFTWARE: FastSEQ for Windows Version 4.0

;

SEQ ID NO 3

;

LENGTH: 410

;

TYPE: PRT

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ORGANISM: Homo sapiens

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US-09-880-137-3

;

Query Match 46.0%; Score 907.5; DB 9; Length 410;

Best Local Similarity 47.2%; Pred. No. 3.7e-76; Mismatches 112; Indels 7; Gaps 4;

Matches 176; Conservative 78; Mismatches 112; Indels 7; Gaps 4;

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Qy 6 KVFKKCAPNGKVTLYMGKRDFFDHFVSGVEPIDGIVVLDEYIRDNRKVFQGIVCSFRYGR 65

Db 7 RVFKKASPNKGKTFYLRHIDYCDPVGIVVEPDYLK-NRKVFGOLATT 65

Qy 66 EEDEVMLNFOKELCILASEQIYPRPEKSDEQTKLQERLLKKIGGSNAIPFTFNISPNAPS 125

Db 66 EDLVLGLTRFKDVLVANVQSFPPAPEDKKPLTRIQLQERLIKULGEHAYPFTFEIPPNLPC 125

;

NUMBER OF SEQ ID NOS: 8

;

SOFTWARE: FastSEQ for Windows Version 4.0

;

SEQ ID NO 3

;

LENGTH: 410

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TYPE: PRT

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ORGANISM: Homo sapiens

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US-09-880-137-3

;

Query Match 46.0%; Score 907.5; DB 9; Length 410;

Best Local Similarity 47.2%; Pred. No. 3.7e-76; Mismatches 112; Indels 7; Gaps 4;

Matches 176; Conservative 78; Mismatches 112; Indels 7; Gaps 4;

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Qy 6 KVFKKCAPNGKVTLYMGKRDFFDHFVSGVEPIDGIVVLDEYIRDNRKVFQGIVCSFRYGR 65

Db 7 RVFKKASPNKGKTFYLRHIDYCDPVGIVVEPDYLK-NRKVFGOLATT 65

Qy 66 EEDEVMLNFOKELCILASEQIYPRPEKSDEQTKLQERLLKKIGGSNAIPFTFNISPNAPS 125

Db 66 EDLVLGLTRFKDVLVANVQSFPPAPEDKKPLTRIQLQERLIKULGEHAYPFTFEIPPNLPC 125

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NUMBER OF SEQ ID NOS: 8

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SOFTWARE: FastSEQ for Windows Version 4.0

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SEQ ID NO 3

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LENGTH: 410

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TYPE: PRT

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ORGANISM: Homo sapiens

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US-09-880-137-3

;

Query Match 46.0%; Score 907.5; DB 9; Length 410;

Best Local Similarity 47.2%; Pred. No. 3.7e-76; Mismatches 112; Indels 7; Gaps 4;

Matches 176; Conservative 78; Mismatches 112; Indels 7; Gaps 4;

;

Qy 6 KVFKKCAPNGKVTLYMGKRDFFDHFVSGVEPIDGIVVLDEYIRDNRKVFQGIVCSFRYGR 65

Db 7 RVFKKASPNKGKTFYLRHIDYCDPVGIVVEPDYLK-NRKVFGOLATT 65

Qy 66 EEDEVMLNFOKELCILASEQIYPRPEKSDEQTKLQERLLKKIGGSNAIPFTFNISPNAPS 125

Db 66 EDLVLGLTRFKDVLVANVQSFPPAPEDKKPLTRIQLQERLIKULGEHAYPFTFEIPPNLPC 125

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NUMBER OF SEQ ID NOS: 8

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SOFTWARE: FastSEQ for Windows Version 4.0

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SEQ ID NO 3

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LENGTH: 410

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TYPE: PRT

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ORGANISM: Homo sapiens

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US-09-880-137-3

;

Query Match 46.0%; Score 907.5; DB 9; Length 410;

Best Local Similarity 47.2%; Pred. No. 3.7e-76; Mismatches 112; Indels 7; Gaps 4;

Matches 176; Conservative 78; Mismatches 112; Indels 7; Gaps 4;

;

Qy 6 KVFKKCAPNGKVTLYMGKRDFFDHFVSGVEPIDGIVVLDEYIRDNRKVFQGIVCSFRYGR 65

Db 7 RVFKKASPNKGKTFYLRHIDYCDPVGIVVEPDYLK-NRKVFGOLATT 65

Qy 66 EEDEVMLNFOKELCILASEQIYPRPEKSDEQTKLQERLLKKIGGSNAIPFTFNISPNAPS 125

Db 66 EDLVLGLTRFKDVLVANVQSFPPAPEDKKPLTRIQLQERLIKULGEHAYPFTFEIPPNLPC 125

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NUMBER OF SEQ ID NOS: 8

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SOFTWARE: FastSEQ for Windows Version 4.0

;

SEQ ID NO 3

;

LENGTH: 410

;

TYPE: PRT

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ORGANISM: Homo sapiens

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US-09-880-137-3

;

Query Match 46.0%; Score 907.5; DB 9; Length 410;

Best Local Similarity 47.2%; Pred. No. 3.7e-76; Mismatches 112; Indels 7; Gaps 4;

Matches 176; Conservative 78; Mismatches 112; Indels 7; Gaps 4;

;

Qy 6 KVFKKCAPNGKVTLYMGKRDFFDHFVSGVEPIDGIVVLDEYIRDNRKVFQGIVCSFRYGR 65

Db 7 RVFKKASPNKGKTFYLRHIDYCDPVGIVVEPDYLK-NRKVFGOLATT 65

Qy 66 EEDEVMLNFOKELCILASEQIYPRPEKSDEQTKLQERLLKKIGGSNAIPFTFNISPNAPS 125

Db 66 EDLVLGLTRFKDVLVANVQSFPPAPEDKKPLTRIQLQERLIKULGEHAYPFTFEIPPNLPC 125

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NUMBER OF SEQ ID NOS: 8

;

SOFTWARE: FastSEQ for Windows Version 4.0

;

SEQ ID NO 3

;

LENGTH: 410

;

TYPE: PRT

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ORGANISM: Homo sapiens

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US-09-880-137-3

;

Query Match 46.0%; Score 907.5; DB 9; Length 410;

Best Local Similarity 47.2%; Pred. No. 3.7e-76; Mismatches 112; Indels 7; Gaps 4;

Matches 176; Conservative 78; Mismatches 112; Indels 7; Gaps 4;

;

Qy 6 KVFKKCAPNGKVTLYMGKRDFFDHFVSGVEPIDGIVVLDEYIRDNRKVFQGIVCSFRYGR 65

Db 7 RVFKKASPNKGKTFYLRHIDYCDPVGIVVEPDYLK-NRKVFGOLATT 65

Qy 66 EEDEVMLNFOKELCILASEQIYPRPEKSDEQTKLQERLLKKIGGSNAIPFTFNISPNAPS 125

Db 66 EDLVLGLTRFKDVLVANVQSFPPAPEDKKPLTRIQLQERLIKULGEHAYPFTFEIPPNLPC 125

;

NUMBER OF SEQ ID NOS: 8

;

SOFTWARE: FastSEQ for Windows Version 4.0

;

SEQ ID NO 3

;

LENGTH: 410

;

TYPE: PRT

;

ORGANISM: Homo sapiens

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US-09-880-137-3

;

Query Match 46.0%; Score 907.5; DB 9; Length 410;

Best Local Similarity 47.2%; Pred. No. 3.7e-76; Mismatches 112; Indels 7; Gaps 4;

Matches 176; Conservative 78; Mismatches 112; Indels 7; Gaps 4;

;

Qy 6 KVFKKCAPNGKVTLYMGKRDFFDHFVSGVEPIDGIVVLDEYIRDNRKVFQGIVCSFRYGR 65

Db 7 RVFKKASPNKGKTFYLRHIDYCDPVGIVVEPDYLK-NRKVFGOLATT 65

Qy 66 EEDEVMLNFOKELCILASEQIYPRPEKSDEQTKLQERLLKKIGGSNAIPFTFNISPNAPS 125

Db 66 EDLVLGLTRFKDVLVANVQSFPPAPEDKKPLTRIQLQERLIKULGEHAYPFTFEIPPNLPC 125

;

NUMBER OF SEQ ID NOS: 8

;

SOFTWARE: FastSEQ for Windows Version 4.0

;

SEQ ID NO 3

;

LENGTH: 410

;

TYPE: PRT

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ORGANISM: Homo sapiens

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US-09-880-137-3

;

Query Match 46.0%; Score 907.5; DB 9; Length 410;

Best Local Similarity 47.2%; Pred. No. 3.7e-76; Mismatches 112; Indels 7; Gaps 4;

Matches 176; Conservative 78; Mismatches 112; Indels 7; Gaps 4;

;

Qy 6 KVFKKCAPNGKVTLYMGKRDFFDHFVSGVEPIDGIVVLDEYIRDNRKVFQGIVCSFRYGR 65

Db 7 RVFKKASPNKGKTFYLRHIDYCDPVGIVVEPDYLK-NRKVFGOLATT 65

Qy 66 EEDEVMLNFOKELCILASEQIYPRPEKSDEQTKLQERLLKKIGGSNAIPFTFNISPNAPS 125

Db 66 EDLVLGLTRFKDVLVANVQSFPPAPEDKKPLTRIQLQERLIKULGEHAYPFTFEIPPNLPC 125

US-09-880-137-1
 Sequence 1, Application US/09880137
 Patent No. US200301295A1
 GENERAL INFORMATION:
 APPLICANT: Bernstein, Gabriel

TITLE OF INVENTION: METHODS OF ASSAYING FOR G CURRENT APPLICATION NUMBER: US/09/880,137

PRIOR APPLICATION NUMBER: MNI-131

CURRENT FILING DATE: 2001-03-05

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 418

TYPE: PRT

ORGANISM: Bos taurus

US-09-880-137-1

Query Match

Best Local Similarity 45.8%; Score 903.5; DB 10; Length 418; Matches 179; Conservative 76; Mismatches 112; Indels 13; Gaps 5;

Qy 6 KVFKKCAPNGKVTLXMGKRDVFVHDVHSVGVVERIDGIVWLDEYIRDNRKVFGQIVCSFRYGR 65
 Db 7 RVFKKASPNKGKLTIVLGKRDVFVHDVLDLVEPVDGVLVLPETYKE-RRVVLTCAFRYGR 65

Qy 66 EDEVMGLNFOKECLASEQIYPRPEKSDEQTKLQERLKKLGSNAIPFTFNISPNA 125
 Db 66 EDLVLGLTFRKDLFVANQSFPPAPEDKKPLTRIQLRERLIKLGEGHAYPFTFEIPPNLPC 125

Qy 126 SVTLQGEDDNGPCGVSYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGOQPC 125
 Db 126 SVTLQGEDDNGPCGVSYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGOQPC 125

Qy 186 VRKDFMLSPGELELEVTLDKOLYLGKRVIGNINICIRNNSNKVKIKAMVQGVDVWLFO 185
 Db 186 VRKDFMLSPGELELEVTLDKOLYLGKRVIGNINICIRNNSNKVKIKAMVQGVDVWLFO 185

Qy 246 NGSYRNTVASLETSEGCPIQPGSSLQKVMYLPLLSNKKRQGIALDGQIKRQDQCLAST 305
 Db 246 TAQKCPVAMEADD--TVAPSSTFCKVYLTPFLANREKRGKLAQDGKLUHEDTNLASS 305

Qy 306 TLLAQPDQDRAFTGVLISYAVKVKLFL--GALGGELSA----ELPFVLMHPKPGTK--A 355
 Db 304 TLLREGANREILGIVSYKVVKLVLSRGGLGDLASSDVAELPFTLMHPKKEEPPHR 363

Qy 356 KVHADSDQADVETFRQDTID 375
 Db 364 EVPBHETPVDTNLIELDTND 383

RESULT 8

US-10-038-010-52

Sequence 52, Application US/10038010

Publication No. US20030040089A1

GENERAL INFORMATION:

APPLICANT: HIBRIGENICS

APPLICANT: Pierre, Legrain

TITLE OF INVENTION: Protein-protein interactions in adipocyte cells

FILE REFERENCE: B4767A

CURRENT APPLICATION NUMBER: US/10/038,010

PRIOR APPLICATION NUMBER: 2002-07-23

PRIOR FILING DATE: 2001-01-02

NUMBER OF SEQ ID NOS: 67

SOFTWARE: PatentIn version 3.1

SEQ ID NO 52

LENGTH: 452

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: beta Arrestin 1

LOCATION: (1)..(452)

OTHER INFORMATION:

RESULT 9

US-10-038-010-52

Sequence 52, Application US/10038010

Publication No. US20030040089A1

GENERAL INFORMATION:

APPLICANT: HIBRIGENICS

APPLICANT: Pierre, Legrain

TITLE OF INVENTION: Protein-protein interactions in adipocyte cells

FILE REFERENCE: B4767A

CURRENT APPLICATION NUMBER: US/10/038,010

PRIOR APPLICATION NUMBER: 2002-07-23

PRIOR FILING DATE: 2001-01-02

NUMBER OF SEQ ID NOS: 67

SOFTWARE: PatentIn version 3.1

SEQ ID NO 52

LENGTH: 452

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: beta Arrestin 1

LOCATION: (1)..(452)

OTHER INFORMATION:

RESULT 8

US-09-800-137A-1

Sequence 1, Application US/09800137A

GENERAL INFORMATION:

APPLICANT: Bernstein, Gabriel

TITLE OF INVENTION: METHODS OF ASSAYING FOR G

FILE REFERENCE: MNI-131

CURRENT APPLICATION NUMBER: US/09/800,137A

PRIOR APPLICATION NUMBER: US/09/800,137A

CURRENT FILING DATE: 2001-03-05

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 418

TYPE: PRT

ORGANISM: Bos taurus

FEATURE:

NAME/KEY: beta Arrestin 1

LOCATION: (1)..(452)

OTHER INFORMATION:

RESULT 9

US-10-038-010-52

Sequence 52, Application US/10038010

Publication No. US20030040089A1

GENERAL INFORMATION:

APPLICANT: HIBRIGENICS

APPLICANT: Pierre, Legrain

TITLE OF INVENTION: Protein-protein interactions in adipocyte cells

FILE REFERENCE: B4767A

CURRENT APPLICATION NUMBER: US/10/038,010

PRIOR APPLICATION NUMBER: 2002-07-23

PRIOR FILING DATE: 2001-01-02

NUMBER OF SEQ ID NOS: 67

SOFTWARE: PatentIn version 3.1

SEQ ID NO 52

LENGTH: 452

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: beta Arrestin 1

LOCATION: (1)..(452)

OTHER INFORMATION:

RESULT 8

US-09-800-137A-1

Sequence 1, Application US/09800137A

GENERAL INFORMATION:

APPLICANT: Bernstein, Gabriel

TITLE OF INVENTION: METHODS OF ASSAYING FOR G

FILE REFERENCE: MNI-131

CURRENT APPLICATION NUMBER: US/09/800,137A

PRIOR APPLICATION NUMBER: US/09/800,137A

CURRENT FILING DATE: 2000-03-03

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 418

TYPE: PRT

ORGANISM: Bos taurus

FEATURE:

NAME/KEY: beta Arrestin 1

LOCATION: (1)..(452)

OTHER INFORMATION:

RESULT 9

US-10-038-010-52

Sequence 52, Application US/10038010

Publication No. US20030040089A1

GENERAL INFORMATION:

APPLICANT: HIBRIGENICS

APPLICANT: Pierre, Legrain

TITLE OF INVENTION: Protein-protein interactions in adipocyte cells

FILE REFERENCE: B4767A

CURRENT APPLICATION NUMBER: US/10/038,010

PRIOR APPLICATION NUMBER: 2002-07-23

PRIOR FILING DATE: 2001-01-02

NUMBER OF SEQ ID NOS: 67

SOFTWARE: PatentIn version 3.1

SEQ ID NO 52

LENGTH: 452

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: beta Arrestin 1

LOCATION: (1)..(452)

OTHER INFORMATION:

RESULT 8

US-09-800-137A-1

Sequence 1, Application US/09800137A

GENERAL INFORMATION:

APPLICANT: Bernstein, Gabriel

TITLE OF INVENTION: METHODS OF ASSAYING FOR G

FILE REFERENCE: MNI-131

CURRENT APPLICATION NUMBER: US/09/800,137A

PRIOR APPLICATION NUMBER: US/09/800,137A

CURRENT FILING DATE: 2000-03-03

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 418

TYPE: PRT

ORGANISM: Bos taurus

FEATURE:

NAME/KEY: beta Arrestin 1

LOCATION: (1)..(452)

OTHER INFORMATION:

RESULT 9

US-10-038-010-52

Sequence 52, Application US/10038010

Publication No. US20030040089A1

GENERAL INFORMATION:

APPLICANT: HIBRIGENICS

APPLICANT: Pierre, Legrain

TITLE OF INVENTION: Protein-protein interactions in adipocyte cells

FILE REFERENCE: B4767A

CURRENT APPLICATION NUMBER: US/10/038,010

PRIOR APPLICATION NUMBER: 2002-07-23

PRIOR FILING DATE: 2001-01-02

NUMBER OF SEQ ID NOS: 67

SOFTWARE: PatentIn version 3.1

Db 126 SVTLQPGPDEDTGKACGVYEVKAFCAEENLEEKIHKRNSVRLVIRKVQYAPERPGPQPTAE 185

Qy 186 VRKDFMLSPGELELEVLTDKOLYLHGERIGVNICIRNNNSNKKIKAMVQGVDVLFQ 245

Db 186 TTRQFLMSDKPLHLEASLDKEIYHGEPISVNVRHTNTKTVKKIKISVRQYADICLFN 245

Qy 246 NGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLLUSSNKQRGGIALDQIKRQDQCLAST 305

Db 246 TAQYKCPVAMEADD--TVAPSSTFCKVYTLTPFLANNREKRGALDGKLIKEDTNCLASS 303

Qy 306 TLLAQPDQDRAFTGVIISYAVKVVLFL--LGALGGELSA----ELPFVLMHPPKGTK--A 355

Db 304 TLLREGANREILGIVSYKVVKVLVSRGGLLGDLASSDVAVELPFTLMHPPKKEEPHR 363

Qy 356 KVTHADSQADVETFRQDTID 375

Db 364 EVPENETPVDTNLIEDTND 383

RESULT 10

US-10-043-487-348

; Sequence 348, Application US/10043487

; Publication No. US20030055220A1

; GENERAL INFORMATION:

; APPLICANT: HYBRIGENICS

; TITLE OF INVENTION: Protein-protein interactions between *Shigella flexneri* polypeptid

; TITLE OF INVENTION: mammalian polypeptides

; FILE REFERENCE: B4778A

; CURRENT APPLICATION NUMBER: US/10/043, 487

; CURRENT FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: US 60/261, 130

; NUMBER OF SEQ ID NOS: 561

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 348

; LENGTH: 418

; TYPE: PRT

; ORGANISM: *Shigella flexneri*

; US-10-043-487-348

Query Match 45.5%; Score 897.5; DB 9; Length 418;

Best Local Similarity 46.8%; Pred. No. 3.3e-75; Mismatches 113; Indels 13; Gaps 5;

Matches 178; Conservative 76; Mismatches 113; Indels 13; Gaps 5;

Qy 6 KVEKKCAPNGKVTLYMGKRDVFVDHVSQVSGVEPIDGIVVLDDEYIRDNRKVFGQIVCSFRYGR 65

Db 7 RVFKKASPNKGKLTIVLGKRDVFVDHIDLPVGDWVLDPEYIKE-RRVYVTLCAFRYGR 65

Qy 66 EEDEVVMGLNFOKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTFNISPNA 125

Db 66 EDLDVUGLTFRKDLFVANVQSFPPAEPDKPLTRIQUERLIKLGHEAYPFTFEIPPNLPC 125

Qy 126 SVTLQPGEDDNGDPCGVSYVVKIPAGESETDRTHRSTVTLGIRKIQFAPTKQGQQPCTL 185

Db 126 SVTLQPGPDEDTGKACGVYEVKAFCAEENLEEKIHKRNSVRLVIRKVQYAPERPGPQPTAE 185

Qy 186 VRKDFMLSPGELELEVLTDKOLYLHGERIGVNICIRNNNSNKKIKAMVQGVDVLFQ 245

Db 186 TTRQFLMSDKPLHLEASLDKEIYHGEPISVNVRHTNTKTVKKIKISVRQYADICLFN 245

Qy 246 NGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLLUSSNKQRGGIALDQIKRQDQCLAST 305

Db 246 TAQYKCPVAMEADD--TVAPSSTFCKVYTLTPFLANNREKRGALDGKLIKEDTNCLASS 303

Qy 306 TLLAQPDQDRAFTGVIISYAVKVVLFL--LGALGGELSA----ELPFVLMHPPKGTK--A 355

Db 304 TLLREGANREILGIVSYKVVKVLVSRGGLLGDLASSDVAVELPFTLMHPPKKEEPHR 363

Qy 356 KVTHADSQADVETFRQDTID 375

Db 364 EVPENETPVDTNLIEDTND 383

RESULT 11

US-09-880-137-2

; Sequence 2, Application US/09880137

; Publication No. US20020031295A1

; GENERAL INFORMATION:

; APPLICANT: Bernstein, Gabriel

; TITLE OF INVENTION: METHODS OF ASSAYING FOR G

; TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS

; FILE REFERENCE: MNI-131

; CURRENT APPLICATION NUMBER: US/09/880, 137

; CURRENT FILING DATE: 2001-03-05

; PRIOR APPLICATION NUMBER: US 60/186, 706

; PRIOR FILING DATE: 2000-03-03

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 418

; TYPE: PRT

; ORGANISM: *Homo sapiens*

US-09-880-137-2

Query Match 45.5%; Score 897.5; DB 9; Length 418;

Best Local Similarity 46.8%; Pred. No. 3.3e-75; Mismatches 113; Indels 13; Gaps 5;

Matches 178; Conservative 76; Mismatches 113; Indels 13; Gaps 5;

Qy 6 KVEKKCAPNGKVTLYMGKRDVFVDHVSQVSGVEPIDGIVVLDDEYIRDNRKVFGQIVCSFRYGR 65

Db 7 RVFKKASPNKGKLTIVLGKRDVFVDHIDLPVGDWVLDPEYIKE-RRVYVTLCAFRYGR 65

Qy 66 EEDEVVMGLNFOKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTFNISPNA 125

Db 66 EDLDVUGLTFRKDLFVANVQSFPPAEPDKPLTRIQUERLIKLGHEAYPFTFEIPPNLPC 125

Qy 126 SVTLQPGEDDNGDPCGVSYVVKIPAGESETDRTHRSTVTLGIRKIQFAPTKQGQQPCTL 185

Db 126 SVTLQPGPDEDTGKACGVYEVKAFCAEENLEEKIHKRNSVRLVIRKVQYAPERPGPQPTAE 185

Qy 186 VRKDFMLSPGELELEVLTDKOLYLHGERIGVNICIRNNNSNKKIKAMVQGVDVLFQ 245

Db 186 TTRQFLMSDKPLHLEASLDKEIYHGEPISVNVRHTNTKTVKKIKISVRQYADICLFN 245

Qy 246 NGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLLUSSNKQRGGIALDQIKRQDQCLAST 305

Db 246 TAQYKCPVAMEADD--TVAPSSTFCKVYTLTPFLANNREKRGALDGKLIKEDTNCLASS 303

Qy 306 TLLAQPDQDRAFTGVIISYAVKVVLFL--LGALGGELSA----ELPFVLMHPPKGTK--A 355

Db 304 TLLREGANREILGIVSYKVVKVLVSRGGLLGDLASSDVAVELPFTLMHPPKKEEPHR 363

Qy 356 KVTHADSQADVETFRQDTID 375

Db 364 EVPENETPVDTNLIEDTND 383

RESULT 12

US-09-800-137A-2

; Sequence 2, Application US/09800137A

; Publication No. US2003015755A1

; GENERAL INFORMATION:

; APPLICANT: Bernstein, Gabriel

; TITLE OF INVENTION: METHODS OF ASSAYING FOR G

; TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS

; FILE REFERENCE: MNI-131

; CURRENT APPLICATION NUMBER: US/09/800, 137A

; CURRENT FILING DATE: 2001-03-05

; PRIOR APPLICATION NUMBER: US 60/186, 706

; PRIOR FILING DATE: 2000-03-03

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 418

; TYPE: PRT

; ORGANISM: Homo sapiens
; US-09-800-137A-2

Query Match
Best Local Similarity 45.5%; Score 897.5; DB 10; Length 418;

Matches 178; Conservative 76; Mismatches 113; Indels 13; Gaps 5;

Qy 6 KVKKCAPNGKVTLYMGKRDVFVHDHSGVVEPIDGIVVULDEYIRDNRKVFGQIVCSFRYGR 65

Db 7 RVFKKASPNCKLTIVLGKRDVFVHDHSGVVEPIDGIVVULDEYIRDNRKVFGQIVCSFRYGR 65

Qy 66 EDEVMGLNFOKECLASEQIVPRPEKSDKEQTQKLERLLKLGNSNAIPFTENISPNA 125

Db 67 EDLVLGLSFRKDLFIATVQAPPVNPNNPPTLQDRLLRKGHAPFFFTIPQNLPC 125

Qy 1.6 SVTLQGEDDNGDPCGVSYWVLFAGESETDRHRSVTILGIRKIQFAPTKQGOQPC 125

Db 1.6 SVTLQGEDDNGDPCGVSYWVLFAGESETDRHRSVTILGIRKIQFAPTKQGOQPC 125

RESULT 13
US-09-800-137-8
; Sequence 8, Application US/09880137
; Patent No. US20020031295A1
; GENERAL INFORMATION:
; APPLICANT: Bernstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; CURRENT APPLICATION NUMBER: MNI-131
; PRIORITY APPLICATION NUMBER: US/09/800,137
; CURRENT FILING DATE: 2001-03-05
; PRIORITY FILING DATE: 2000-03-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence

US-09-800-137-8

Query Match
Best Local Similarity 45.5%; Score 897.5; DB 10; Length 418;

Matches 178; Conservative 76; Mismatches 113; Indels 13; Gaps 5;

Qy 6 KVKKCAPNGKVTLYMGKRDVFVHDHSGVVEPIDGIVVULDEYIRDNRKVFGQIVCSFRYGR 65

Db 7 RVFKKASPNCKLTIVLGKRDVFVHDHSGVVEPIDGIVVULDEYIRDNRKVFGQIVCSFRYGR 65

Qy 66 EDEVMGLNFOKECLASEQIVPRPEKSDKEQTQKLERLLKLGNSNAIPFTENISPNA 125

Db 67 EDLVLGLSFRKDLFIATVQAPPVNPNNPPTLQDRLLRKGHAPFFFTIPQNLPC 125

Qy 1.6 SVTLQGEDDNGDPCGVSYWVLFAGESETDRHRSVTILGIRKIQFAPTKQGOQPC 125

Db 1.6 SVTLQGEDDNGDPCGVSYWVLFAGESETDRHRSVTILGIRKIQFAPTKQGOQPC 125

RESULT 14
US-09-800-137A-8
; Sequence 8, Application US/09800137A
; Publication No. US20030157553A1
; GENERAL INFORMATION:
; APPLICANT: Bernstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; CURRENT APPLICATION NUMBER: MNI-131
; PRIORITY APPLICATION NUMBER: US/09/800,137A
; CURRENT FILING DATE: 2001-03-05
; PRIORITY FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence

US-09-800-137A-8
Query Match
Best Local Similarity 44.9%; Score 885; DB 10; Length 382;

Matches 167; Conservative 48.3%; Pred. No. 4.3e-74; Mismatches 98; Indels 4; Gaps 3;

Qy 6 KVKKCAPNGKVTLYMGKRDVFVHDHSGVVEPIDGIVVULDEYIRDNRKVFGQIVCSFRYGR 65

Db 8 RVFKKASPNCKLTIVLGKRDVFVHDHSGVVEPIDGIVVULDEYIRDNRKVFGQIVCSFRYGR 66

Qy 66 EDEVMGLNFOKECLASEQIVPRPEKSDKEQTQKLERLLKLGNSNAIPFTENISPNA 125

Db 67 EDLVLGLSFRKDLFIATVQAPPVNPNNPPTLQDRLLRKGHAPFFFTIPQNLPC 125

Qy 1.6 SVTLQGEDDNGDPCGVSYWVLFAGESETDRHRSVTILGIRKIQFAPTKQGOQPC 125

Db 1.6 SVTLQGEDDNGDPCGVSYWVLFAGESETDRHRSVTILGIRKIQFAPTKQGOQPC 125

RESULT 15
US-09-800-137-4
; Sequence 4, Application US/09880137
; Patent No. US20020031295A1
; GENERAL INFORMATION:
; APPLICANT: Bernstein, Gabriel

```

; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
; FILE REFERENCE: MNI-131
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-880-137-4

Query Match          44.9%;  Score 885;  DB 9;  Length 409;
Best Local Similarity 48.3%;  Pred. No. 4.7e-74;
Matches 167;  Conservative 77;  Mismatches 98;  Indels 4;  Gaps 3;
Oy      6 KVEKKCAPNGKVLYMGRDFDVFHSGVEPIRGIVVLDDEYIRDNRKVFGQIVCSFRYGR 65
Db      8 RVFKKSSPNCKLTVLGRDFDVLKDPVGVWLVDPDYLKD-RKVFTVLTCAFRYGR 66
Oy      66 EEDEVVMGLNFOKEELCLASEQTYPRPEKSDEQTKLQERLLKKLGSNAIPFTFNISPNA 125
Db      67 EDLDVLGLSFRKDLFIATYQAFPPVNPFRPPTRLQDRLLRKLGQAHAPFFFTIPQNLPC 126
Oy      126 SVTLOQGEDDNGDPGCVSYVKIFAGESETDRTHRSTVTLGRKIQFAPTKQGQOOPCTL 185
Db      127 SVTLQGPEDTGKACGVDFEIRAFCAKSLEEKSHKRNVRVLRKQFAPEKPGQPSAE 186
Oy      186 VRKDFMLSPGELELEVILDQQLXHGERIGVNICIRANSNRMKKIKAMVOQGVVLFQ 245
Db      187 TTRHFLMSDRSLHLEASLDKELYYHGEPILAVNVHVTNNSTKTVKKIKVSVRQYADICLFS 246
Oy      246 NGSYRNTVASLETSEGCPIQPGSSLQKMYLTPULLSNKQRGIGLDQIKRQDQCLAST 305
Db      247 TAQYKCPVAQLEDD-QVSPSSTFCCKYTTPLLSNDREKRGALDGKLIKEDTNLAS 304
Oy      306 TLLAQPDQDRAFTGVIISYAVKVKLFLGALGGEELSAELPFVLMHPKP 351
Db      305 TIVKEGANKEVVLGILVSYRKVKLWV-SRGGDVSVELPFVLMHPKP 349

```

Search completed: February 9, 2005, 23:44:23
 Job time : 132 sec

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GenCore version 5.1.6
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Om protein - protein search, using sw model

Run on: February 9, 2005, 23:45:38 ; Search time 165 seconds
 (without alignments)
 897.753 Million cell updates/sec

Title: US-10-056-405-2
 Perfect score: 383
 Sequence: 1 MVYNFKVFKKCAPNGKVTLY.....ADVETFRODTIDQCCASWDDE 383

Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqB, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_16Dec04;*
 1: geneseqp1980s;*
 2: geneseqp1990s;*
 3: geneseqp2000s;*
 4: geneseqp2001s;*
 5: geneseqp2002s;*
 6: geneseqp2003as;*
 7: geneseqp2003bs;*
 8: geneseqp2004s;*

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

26 8 2.1 38 4 ABB25470
 27 8 2.1 38 4 AAM75381
 28 8 2.1 38 4 AAM62570
 29 8 2.1 38 4 ABG57138
 30 8 2.1 38 5 ABG44975
 31 8 2.1 180 6 ADA00634
 32 8 2.1 182 7 ADD27419
 33 8 2.1 182 7 ADD27127
 34 8 2.1 182 7 ADD27197
 35 8 2.1 187 6 ABU70623
 36 8 2.1 187 7 ADD27059
 37 8 2.1 204 2 AAW24688
 38 8 2.1 212 4 AAG73899
 39 8 2.1 279 7 ABO78668
 40 8 2.1 315 6 ADA00636
 41 8 2.1 360 6 ADA00635
 42 8 2.1 366 2 AAW20643
 43 8 2.1 369 4 ABG13574
 44 8 2.1 405 4 AAM78763

RESULT 1
 ID ABP52833
 ID ABP52833 standard; protein; 383 AA.
 XX
 AC ABP52833;
 XX
 DT 01-NOV-2002 (first entry)
 XX
 DE Anopheles gambiae arrestin 1 protein SEQ ID NO:2.
 XX
 KW Anopheles gambiae; mosquito; olfactory gene; arrestin 1; pest control; odourant receptor; olfaction.
 KW
 OS Anopheles gambiae.
 OS
 XX
 PN WO200259274-A2.
 XX
 PD 01-AUG-2002.
 XX
 PP 28-JAN-2002; 2002WO-US002549.
 XX
 PR 26-JAN-2001; 2001US-0264649P.
 PR 24-JAN-2002; 2002US-00056405.
 XX
 PA (UYVA-) UNIV VANDERBILT.
 XX
 PI Zwiebel LJ;
 XX
 DR WPI; 2002-627421/67.
 DR N-PSDB; ABQ75102.

XX
 PT New mosquito olfaction polypeptides and polynucleotides, useful for mosquito management, i.e. controlling the pest and disease vectors, or for identifying pest control agents.
 PT
 XX
 PS Claim 18; Fig 2; 96pp; English.

XX
 CC
 The present invention describes a purified Anopheles gambiae olfaction polypeptide comprising a 383, 394, 380, 411, 412, 391, 157 or 401 residue amino acid sequence (see ABP52833 to ABP52840) (S1), a conservatively modified amino acid sequence of them, or a sequence of (S1) with at least 20 consecutive residues. Also described: (1) an isolated polynucleotide comprising: (a) a nucleotide sequence encoding the purified Anopheles gambiae olfaction polypeptide; or (b) a nucleotide sequence that hybridises under stringent conditions to a hybridisation probe comprising a 1964, 1239, 1142, 1236, 1194, 1176, 474 or 1206 nucleotide sequence (see ABQ75102 to ABQ75105 and ABQ75110 to ABQ75113) (S2), or its complement; and (2) a method for identifying an agent that binds to

CC isolated --action molecule, (b) --ing: (a) providing an isolated CC of the test agent to the isolated molecule; and (c) detecting specific CC olfaction-binding identifies the olfaction molecule, where "bind- CC ing" means the ability of the test agent to bind to the isolated molecule.

N-PSDB; ACF79716.

Claim 1; Fig 2; 101pp; English.
The present invention relates to a method for reducing the incidence of bloodmeal, e.g. humans.

Best Local Similarity 100.0%; Score 383; DB 5; Length 383;
 Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Local Similarity 100.0%; Pred. No. 0;
 1 MVVNFKVFKKCAPNGKVTLMGKRPDVHDVSGVERPDGIVLDDDEYIRDNRKVFQGIVCS 60
 1 MVVNFKVFKKCAPNGKVTLMGKRPDVHDVSGVERPDGIVLDDDEYIRDNRKVFQGIVCS 60
 61 FRYQGKREDEEVNGINFOKELCLASEOYPRPEKSDEQTKLQERLKKLGSNAIPFTFNIS 60
 61 FRYQGKREDEEVNGINFOKELCLASEOYPRPEKSDEQTKLQERLKKLGSNAIPFTFNIS 60
 121 PNAPASSVTLQQGEDDNGDPGCVSYVVKIFAGESETDRTHRPSSTMGNSAIPFTFNIS 120
 121 PNAPASSVTLQQGEDDNGDPGCVSYVVKIFAGESETDRTHRPSSTMGNSAIPFTFNIS 120

QY	181	QPCTLVRKDFMLSPGEGELELEVTLDKQLYLHGERIGVNICIRNNSNKVKITKAMVOQVD
Db	181	QPCTLVRKDFMLSPGEGELELEVTLDKQLYLHGERIGVNICIRNNSNKVKITKAMVOQVD
Qy	240	WLFQONGSYRNTVASLETSEGCPROPGESIQRKUMLTPLISSNKQRGIALDGOIKRQDO
Db	240	VVLFONGSYRNTVASLETSEGCPROPGESIQRKUMLTPLISSNKQRGIALDGOIKRQDO
Qy	300	CLASTTLIAQPQDQDRAFTVLSLETSEGCPQPGSSLQKVMYLTPLLSNKQRGIALDGQIKRQDO
Db	300	CLASTTLIAQPQDQDRAFTVLSLETSEGCPQPGSSLQKVMYLTPLLSNKQRGIALDGQIKRQDO
Qy	360	DSQADVENTFRQDTIDQASVDFE
Db	360	DSQADVENTFRQDTIDQASVDFE
	383	DSQADVENTFRQDTIDQASVDFE
	361	DSQADVENTFRQDTIDQASVDFE

Query Match		Best Local Similarity		Score		DB		Length	
Qy	Matches	383;	Conservative	100.0%	383	Pred.	No.	7	383
				0;	Mismatches	0;	Indels	0;	Gaps
1	MVYNEFKVKKCAPNGKVTLYNGKRD	F	DHVSGVERPIDGIWIL	D	VLD	DEYIRDNRKVFGOIVCS	60		
1	MVYNEFKVKKCAPNGKVTLYNGKRD	F	DHVSGVERPIDGIWIL	D	VLD	DEYIRDNRKVFGOIVCS	60		
61	FRYGRBEEDEVMGLNFOKELCLASEQIYPRPEKS	IY	YDKEQTKLQERLILKLG	SNAI	IPFTFNIS	60			
61	FRYGRBEEDEVMGLNFOKELCLASEQIYPRPEKS	IY	YDKEQTKLQERLILKLG	SNAI	IPFTFNIS	60			
121	PNAPSSVTLOQGEDDNGDPCCGVSYYVKI	FAGESETDR	THRRSTVTLGIRKIQ	FAPTKOGO	180				
121	PNAPSSVTLOQGEDDNGDPCCGVSYYVKI	FAGESETDR	THRRSTVTLGIRKIQ	FAPTKOGO	180				

RESULT	2
ABR84476	
ID	ABR84476
XX	standard; protein; 383 AA.
AC	ABR84476;
XX	
DT	
XX	15-JAN-2004 (first entry)
DE	Mosquito olfaction molecule, arrestin 1.
XX	
KW	Arrestin 1; mosquito; olfaction; insecticide; antimalarial.
XX	
OS	<i>Anopheles gambiae</i> .
XX	

181 QPCTLVRKDFMLSPGELEVTLDKOLYLGERTIGVNICIRNSNKVCKTAKAMVQGVD 180
 241 VVLFPQNSYRNTVASLETSSEGCP1OPGSS1QKOMVLTPLLSNKQRRGIALDGQIKRQDQ 240
 241 VVLFRQNGSYRNTVASLETSEGCP1QPGSS1QKOMVLTPLLSNKQRRGIALDGQIKRQDQ 240
 301 CLASTTLLAQPDQDAFGVITISYAVVKVLFGLALGGELSAELPFVIMMPKCTKAKVTHA 300
 301 CLASTTLLAQPDQDAFGVITISYAVVKVLFGLALGGELSAELPFVIMMPKCTKAKVTHA 300
 361 DSQADQVETFRQDTIDQOASVDFE 360
 361 DSQADQVETFRQDTIDQOASVDFE 360
 361 DSQADQVETFRQDTIDQOASVDFE 360

XX
PD
XX
18-SEP-2003.
PP
XX
10-MAR-2003; 2003WO-US007174.
PR
08-MAR-2002; 2002US-00094240.
XX
PA
(UVVA-) UNIV VANDERBILT.
XX
PI
Zwiebel LJ;
XX

PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 PT
 PR XX 23-MAR-2001; 2001WO-US009231.
 PT
 PR XX 23-MAR-2000; 2000US-0191637P.
 PT
 PR XX 11-JUL-2000; 2000US-00614150.
 PS
 PA (PEKE) PE CORP NY.
 XX
 PT Venter JC, Adams M, Li PWD, Myers EW;
 XX DR WPI; 2001-656860/75.
 N-PSDB; ABL05839.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from *Drosophila* and for elucidating cell signaling and cell-cell interactions.
 PT
 PS Disclosure; SEQ ID NO 12000; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from *Drosophila*. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 364 AA;
 CC
 CC Best Local Similarity 100.0%; Pred. No. 1.2e-10;
 CC Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 Oy 228 VKKIKAMVQQGVDFVLFONG 247
 Db 227 VKKIKAMVQQGVDFVLFONG 246
 XX
 RESULT 5
 AAG67785
 ID AAG67785 standard; protein; 382 AA.
 XX
 AC AAG67785;
 XX DT 10-DEC-2001 (first entry)
 XX DE An exemplary phosphorylation-independent arrestin mutant.
 XX
 ADQ89588
 ID ADQ89588 standard; protein; 364 AA.
 XX AC ADQ89588;
 XX DT 21-OCT-2004 (first entry)
 XX DE Antagonist of cell cycle progression polypeptide #9.
 XX KW Cytostatic; cancer; cell division cycle; mitosis; meiosis; cell cycle progression.
 XX OS *Drosophila melanogaster*.
 XX PN WO2004063362-A2.
 XX PD 29-JUL-2004.
 XX PP 31-DEC-2003; 2003WO-GB005635.
 XX PR 10-JAN-2003; 2003US-0439123P.
 PR 06-MAY-2003; 2003US-0468402P.
 XX PA (CYCL-) CYCLACEL LTD.
 XX PT Glover D, Bell G, Frenz L, Midgley C;
 XX DR WPI; 2004-544089/52.
 XX
 DR N-PSDB; ADQ89587.
 XX
 PT New cell cycle progression genes and proteins for modulating cell cycle progression in cells, for preventing, treating or diagnosing cell proliferative diseases (e.g. cancer) or for identifying modulators of cell cycle progression.
 PT
 PR XX mitosis or meiosis.
 XX PS Claim 2; SEQ ID NO 18; 461pp; English.
 XX
 CC The present invention relates to a polynucleotide for preventing, treating or diagnosing a disease in an individual. The composition or the polypeptide, polynucleotide or RNA precursor, or antibody is useful for diagnosing, preventing or treating diseases (e.g. cell proliferative diseases such as cancer) in an individual. These may also be used for identifying substances capable of binding to or modulating the function of the polypeptide, capable of affecting the function of the corresponding gene, or capable of inhibiting the cell division cycle or cell cycle progression, preferably mitosis and/or meiosis. The present sequence represents an antagonist of cell cycle progression protein sequence.
 CC
 CC Sequence 364 AA;
 CC
 CC Best Local Similarity 100.0%; Pred. No. 1.2e-10;
 CC Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 Oy 228 VKKIKAMVQQGVDFVLFONG 247
 Db 227 VKKIKAMVQQGVDFVLFONG 246
 XX
 RESULT 5
 AAG67785
 ID AAG67785 standard; protein; 382 AA.
 XX
 AC AAG67785;
 XX DT 10-DEC-2001 (first entry)
 XX DE An exemplary phosphorylation-independent arrestin mutant.
 XX
 ADQ89588
 ID ADQ89588 standard; protein; 364 AA.
 XX AC ADQ89588;
 XX DT 21-OCT-2004 (first entry)
 XX DE Antagonist of cell cycle progression polypeptide #9.
 XX KW Cytostatic; cancer; cell division cycle; mitosis; meiosis; cell cycle progression.
 XX OS *Drosophila melanogaster*.
 XX PN WO2004063362-A2.
 XX PD 29-JUL-2004.
 XX PP 31-DEC-2003; 2003WO-GB005635.
 XX PR 10-JAN-2003; 2003US-0439123P.
 PR 06-MAY-2003; 2003US-0468402P.
 XX PA (CYCL-) CYCLACEL LTD.
 XX PT Glover D, Bell G, Frenz L, Midgley C;
 XX DR WPI; 2004-544089/52.
 XX
 DR Identifying a G protein-coupled receptor ligand, useful for treating e.g. retinitis pigmentosa, color blindness or neurological disorders, uses phosphorylation-independent arrestin mutants particularly suited for in vitro screening assays.
 XX
 PS Disclosure; Page 47; 47pp; English.
 XX
 CC The present sequence represents an exemplary phosphorylation-independent

CC arrestin mutant. Such mutants are used in screening assays to identify CC ligands and/or modulators of G protein-coupled receptors (GPCRs). A CC method for identifying a GPCR ligand comprises contacting a composition comprising the GPCR and a constitutively active arrestin mutant with a CC test compound; and determining the ability of the test compound to CC modulate binding of arrestin mutant to the GPCR, where modulation to CC binding indicates that the test compound is a GPCR ligand. The method is CC used for identifying potential ligands and/or modulators of GPCRs, particularly modulators, for use as human therapeutics. Modulators of CC GPCR may be used for treating patients having e.g. retinitis pigmentosa, CC stationary night blindness, colour blindness, nephrogenic DI, isolated CC glucocorticoid deficiency, hyperfunctioning thyroid adenomas, familial CC hypocalciuric hypercalcemia, hyperparathyroidism and neurological CC disorders. The methods may be used for screening pluralities of test CC compounds (e.g. a small molecule library of compounds) or a composition CC containing a plurality of GPCRs. The methods may be used in screening GPCRs, and for identification of natural and surrogate agonists of orphan XX CC GPCR antagonists and/or agonists.

SQ Sequence 382 AA;

Query Match Best Local Similarity 2.9%; Score 11; DB 4; Length 382; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 341 ELPFVLMHPKP 351
Db 339 ELPFVLMHPKP 349

RESULT 6

ABR84484
ID ABR84484 standard; protein; 398 AA.
XX
AC ABR84484;
XX
DT 15-JAN-2004 (first entry)
XX
DE Mosquito olfaction molecule, arrestin 2.
XX
KW Arrestin 2; mosquito; olfaction; insecticide; antimarial.
XX
OS Anopheles gambiae.
XX
FH Key Location/Qualifiers
FT Misc-difference 152
FT /note= "Encoded by AG"
XX
PN WO2003076590-A2.
XX
PD 18-SEP-2003.
XX
PF 10-MAR-2003; 2003WO-US007174.
XX
PR 08-MAR-2002; 2002US-00094240.
XX
PA (UVA-) UNIV VANDERBILT.
XX
PI Zwiebel LJ;
XX
DR WPI; 2003-722331/68.
XX
N-PSDB; ACF79731.

PT New mosquito arrestin 1 and 2 genes and polypeptides, useful for identifying mosquito arrestin 1 and 2 genes and polypeptides, useful for the ability of mosquitoes to locate sources of bloodmeal, e.g. humans. PS Claim 16; Fig 12b; 101pp; English.
CC The present sequence is the protein sequence of arrestin 2, a novel mosquito olfaction molecule. The invention provides 9 novel mosquito polypeptides and the nucleic acids encoding them. These are arrestins 1 and 2 and odorant receptor molecules 1-7. The odorant receptors function

CC in a ligand-induced signal transduction pathway for the activation of CC mosquito olfaction. Arrestin functions to inhibit the activation of CC transduction cascade. Thus, the odorant receptors act as an 'on' switch CC and arrestin as an 'off' switch for the odorant detection system of the mosquito. Methods are provided for identifying compounds that interfere CC with the operation of the mosquito olfactory system, particularly by reducing their ability to locate CC compounds that modulate arrestin 2 activity. These are useful for the control of mosquitoes, particularly by reducing their ability to locate CC sources of bloodmeal.

SQ Sequence 398 AA;

Query Match Best Local Similarity 2.9%; Score 11; DB 7; Length 398; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 62 RYGRGEEDEVMG 72
Db 61 RYGRGEEDEVMG 71

RESULT 7

ABB61964
ID ABB61964 standard; protein; 401 AA.
XX
AC ABB61964;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 12684.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PP 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
XX
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE) PE CORP NY.
XX
PT Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
XX
DR N-PSDB; ABL0607.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
XX
PS Disclosure; SEQ ID NO 12684; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences and pharmaceutical drugs. The invention
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABL16176-ABL30511) expressed DNA
CC (ABL2072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 401 AA;

Query Match Best Local Similarity 2.9%; Score 11; DB 4; Length 401;

Matches	11;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	Qy	341	ELPFVLMHPKP	351		
Qy	62	RYGRRDEEVNG	72							Db	339	ELPFVLMHPKP	349		
Db	61	RYGRRDEEVNG	71												
RESULT 8										RESULT 9					
AAG67784										AAG67781					
ID	AAG67784	standard;	protein;	409	AA.					ID	AAG67781	standard;	protein;	409	AA.
XX										XX					
AC										AC					
XX										XX					
DT	10-DEC-2001	(first entry)								DT	10-DEC-2001	(first entry)			
XX										XX					
DE	An exemplary phosphorylation-independent arrestin mutant.									DE	Amino acid sequence of human beta-arrestin 2.				
XX										XX					
KW	Arrestin; phosphorylation-independent arrestin mutant;									KW	Arrestin; phosphorylation-independent arrestin mutant;				
KW	G protein-coupled receptor; GPCR; GPCR ligand; retinitis pigmentosa;									KW	G protein-coupled receptor; GPCR; GPCR ligand; retinitis pigmentosa;				
KW	stationary night blindness; colour blindness; nephrogenic DI;									KW	stationary night blindness; colour blindness; nephrogenic DI;				
KW	isolated glucocorticoid deficiency; hyperfunctioning thyroid adenoma;									KW	isolated glucocorticoid deficiency; hyperfunctioning thyroid adenoma;				
KW	familial hypocalciuric hypercalcemia; hyperparathyroidism;									KW	familial hypocalciuric hypercalcemia; hyperparathyroidism;				
KW	neurological disorder.									KW	neurological disorder.				
XX										XX					
OS	Unidentified.									OS	Homo sapiens.				
XX										XX					
PN	WO200167106-A2.									PN					
XX										XX					
PD	13-SEP-2001.									PD	13-SEP-2001.				
XX										XX					
PP	05-MAR-2001; 2001WO-US007304.									PP	05-MAR-2001; 2001WO-US007304.				
XX										XX					
PR	03-MAR-2000; 2000US-0186706P.									PR	03-MAR-2000; 2000US-0186706P.				
XX										XX					
PA	(MILL-) MILLENNUM PHARM INC.									PA	(MILL-) MILLENNUM PHARM INC.				
XX										XX					
PI	Berstein G;									PI	Berstein G;				
XX										XX					
DR	WPI; 2001-602637/68.									DR	WPI; 2001-602637/68.				
XX										XX					
XX	Identifying a G protein-coupled receptor ligand, useful for treating e.g. retinitis pigmentosa, color blindness or neurological disorders, uses PT vitro screening assays.									XX	Identifying a G protein-coupled receptor ligand, useful for treating e.g. retinitis pigmentosa, color blindness or neurological disorders, uses PT vitro screening assays.				
PS	Disclosure; Page 47; 47pp; English.									PS	Disclosure; Page 46; 47pp; English.				
XX										XX					
CC	The present sequence represents an exemplary phosphorylation-independent arrestin mutant. Such mutants are used in screening assays to identify ligands and/or modulators of G protein-coupled receptors (GPCRs). A method for identifying a GPCR ligand comprises contacting a composition comprising the GPCR and a test compound; and determining the ability of the test compound to modulate binding of arrestin mutant to the GPCR, where modulation of binding indicates that the test compound is a GPCR ligand. The method is used for identifying potential ligands and/or modulators of GPCRs, particularly modulators, for use as human therapeutics. Modulators of GPCR may be used for treating patients having e.g. retinitis pigmentosa, stationary night blindness, colour blindness, nephrogenic DI, isolated glucocorticoid deficiency, hyperfunctioning thyroid adenomas, familial hypocalciuric hypercalcemia, hyperparathyroidism and neurological disorders. The methods may be used in screening assays for identification of natural and surrogate agonists of orphan GPCRs, and for identification of GPCR antagonists and/or agonists									CC	The present sequence represents an arrestin protein. The specification describes phosphorylation-independent arrestin mutants. These mutants are used in screening assays to identify ligands and/or modulators of G protein-coupled receptors (GPCRs). A method for identifying a GPCR ligand comprises contacting a composition comprising the GPCR and a test compound; and determining the ability of the test compound to modulate binding of arrestin mutant to the GPCR, where modulation of binding indicates that the test compound is a GPCR ligand. The method is used for identifying potential ligands and/or modulators of GPCRs, particularly modulators, for use as human therapeutics. Modulators of GPCR may be used for treating patients having e.g. retinitis pigmentosa, stationary night blindness, colour blindness, nephrogenic DI, isolated glucocorticoid deficiency, hyperfunctioning thyroid adenomas, familial hypocalciuric hypercalcemia, hyperparathyroidism and neurological disorders. The methods may be used for screening pluralities of test compounds (e.g. a small molecule library of compounds) or a composition containing a plurality of GPCRs. The methods may be used in screening assays for identification of natural and surrogate agonists of orphan GPCRs, and for identification of GPCR antagonists and/or agonists				
CC	sequence 409 AA;									CC	sequence 409 AA;				
CC	Query Match 2.9%; Score 11; DB 4; Length 409;									CC	Query Match 2.9%; Score 11; DB 4; Length 409;				
CC	Best Local Similarity 100.0%; Pred. No. 0.11;									CC	Best Local Similarity 100.0%; Pred. No. 0.11;				
CC	Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									CC	Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				

Qy	Conservative			0; Mismatches - - , 0; Indels			0; Gaps 0;		
341	ELPFVLMHPKP	351							
339	ELPFVLMHPKP	349							

Sequence 409 AA;

RESULT 10
ADE58183
ID ADE58183 standard; protein; 409 aa.
XX
AC ADE58183;
XX
DT 29-JAN-2004 (first entry)
XX

Best Local Similarity 100.0%; Score 11; DB 7; Length 409;
 Matches 11; Conservative 0; Pred. No. 0.11; Mismatches 0;
 QY 341 ELPFVLMHPKP 351 0; Indels 0; Gaps 0;
 Db 339 ELPFVLMHPKP 349

CC or human polynucleotides or a polynucleotide comprising two or more isolated rat
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a compound that regulates
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC

CC injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp://wipo.int/pub/published_pct_sequences.

XX Sequence 409 AA;

Query Match 2.9%; Score 11; DB 7; Length 409;
Best Local Similarity 100.0%; Pred. No. 0.11; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 341 ELPFVLMHPKP 351
Db 339 ELPFVLMHPKP 349

RESULT 12

ADN95251
ID ADN95251 standard; protein; 409 AA.
XX
AC XX
DT XX
DE Human BEC/LEC-related protein sequence SeqID173.

XX growth; differentiation; blood endothelial cell; BEC;
KW lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-3;
KW lymphatic growth agent; VEGF-C; VEGF-D; antiangiogenic; cytostatic;
KW vasoconstrictor; antiinflammatory; gene therapy; endothelial cell disorder;
KW inflammatory disease; cancer metastasis; lymphatic system; human.
XX Homo sapiens.
OS XX
PN WO2003080640-A1.
XX
PD 02-OCT-2003.
XX
PR 07-MAR-2003; 2003WO-US006900.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICHN) LICENTIA LTD.
XX
PI Alitalo K, Makinen T, Petrova T, Saharinen P, Saharinen J;
XX
DR WPI; 2003-876899/81.
XX
DR N-PSDB; ADN95252.
XX
PS Example 1; SEQ ID NO 173; 176pp; English.

XX This invention relates to a method of differentially modulating the growth or differentiation of blood endothelial cells (BEC) or lymphatic endothelial cells (LEC) comprises contacting endothelial cells with a composition comprising an agent that differentially modulates blood or lymphatic endothelial cells. Treating hereditary lymphoedema comprises identifying a human subject with lymphoedema and with a mutation in at least one allele of a gene encoding a LEC protein, where the mutation correlates with lymphoedema in human subjects, and with the proviso that the LEC protein is not VEGFR-3; and administering to the subject a composition comprising a lymphatic growth agent selected from VEGF-C or VEGF-D polypeptides and polynucleotides. The invention may be useful for the development of compounds with an antiangiogenic, cytostatic, vasoconstrictor or antiinflammatory activity or for gene therapy. The method is useful in modulating the growth or differentiation of blood endothelial cells or lymphatic endothelial cells, in treating hereditary lymphoedema, in screening for an endothelial cell disorder or predisposition to the disorder or in monitoring the efficacy or toxicity of a drug on endothelial cells. The agent is useful in manufacturing a medicament for the differential modulation of blood vessel endothelial

CC cell or lymphatic vessel endothelial cell growth or differentiation. The CC lymphatic growth agent may also be used in manufacturing a medicament for CC the treatment of hereditary lymphoedema resulting from a mutation in a CC LEC gene or of other diseases involving the lymphatic vessels, such as CC various inflammatory diseases and cancer metastasis via the lymphatic CC system. The present sequence is that of a human LEC/BEC differentially CC expressed protein which is related to the method of the invention. Note: CC This sequence does not appear in the specification but was obtained by CC the indexer using the source data given in table 14 of the specification.

Query Match 2.9%; Score 11; DB 7; Length 409;
Best Local Similarity 100.0%; Pred. No. 0.11; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 341 ELPFVLMHPKP 351
Db 339 ELPFVLMHPKP 349

RESULT 13

ABG69496
ID ABG69496 standard; protein; 410 AA.
XX
AC ABG69496;
XX
DT 21-OCT-2002 (first entry)
XX
DE Rat bait protein beta arrestin 2.
XX
PR Rat; yeast two-hybrid assay; adipocyte; bait protein; NIDDM;
KW non-insulin diabetes mellitus; obesity; selected interacting domain; SID;
KW protein-protein interaction map; PIM; anorectic; metabolic disorder;
XX
OS XX
PN WO200253726-A2.
XX
PD 11-JUL-2002.
XX
PR 28-DEC-2001; 2001WO-EP015423.
XX
PR 02-JAN-2001; 2001US-0259377P.
XX
PA (HYBR-) HYBRIGENICS.
PA (CNRS) CENT NAT RECH SCI.
XX
PI Legrain P, Marullo S, Jockers R;
XX
DR WPI; 2002-583612/62.
DR N-PSDB; ABS51032.

XX Novel complex of protein-protein interactions in adipocyte cells for PT identifying compounds that modulate the protein-protein interactions and PT useful for treating obesity and metabolic disorders.
XX
PS Claim 1; Page 53; 125pp; English.

XX The invention relates to a complex of protein-protein interactions CC (forming a protein-protein interaction map, PIM) in adipocyte cells as CC defined in the specification, or polynucleotides in adipocytes encoding CC for the polypeptides. Also included are a recombinant cell expressing the CC interacting polypeptides and a method of selecting a modulating compound CC in adipocyte cells, by cultivating a recombinant host cell on a selective CC medium containing a modulating compound and a reporter gene the CC expression of which is toxic for the recombinant host cell which is CC transformed with two vectors, where the first vector comprises a CC polynucleotide encoding a first hybrid polypeptide and DNA binding domain CC and the second vector comprising a polynucleotide encoding a second CC hybrid polypeptide and an activating domain that activates the toxic CC reporter gene, when the first and second hybrid polypeptides interact and CC selecting the modulating compound which inhibits the growth of the CC

CC recombinant host cell (i.e. using the yeast two-hybrid system). The CC complexes are useful for identifying compounds that modulate the protein- CC disorders e.g. non-insulin dependent diabetes mellitus and metabolic CC compound isolated by the method is useful for treating obesity and metabolic CC obesity or metabolic diseases. The present invention, used as the bait protein in the complex further define a set of selected interacting domains, SID. CC invention, used as the bait protein in the yeast two-hybrid assay

SQ Sequence 410 AA;

Query Match
Best Local Similarity 2.9%; Score 11; DB 5; Length 410;
Matches 11; Conservative 0; Pred. No. 0.11; Mismatches 0; Indels 0; Gaps 0;

Qy 341 ELPFVLMHPKP 351
Db 340 ELPFVLMHPKP 350

RESULT 14

ID ADE58177
XX ADE58177 standard; protein; 410 AA.

AC ADE58177;
XX

DT 29-JAN-2004 (first entry)
XX

DE Rat Protein P29067, SEQ ID NO 4048.
XX

KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
OS Rattus norvegicus.
XX

PN WO2003016475-A2.
XX

PD 27-FEB-2003.
XX

PF 14-AUG-2002; 2002WO-US025765.
XX

PR 14-AUG-2001; 2001US-0312147P.
XX 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX

PA (GEHO) GEN HOSPITAL CORP.
(FARB) BAYER AG.
XX

PI Woolf C, D'urso D, Befort K, Costigan M;
XX

PS WPI; 2003-268312/26.
DR GENBANK; P29067.
XX

PT New composition preparing a medicament comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.

CC Claim 1; Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising a vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of the polynucleotide sequence
CC subjected to pain, a method for identifying an agent
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition
CC subjected to pain, a method for identifying a compound which regulates

RESULT 15

ID ADE58181
XX ADE58181 standard; protein; 410 AA.

AC ADE58181;
XX

DT 29-JAN-2004 (first entry)
XX

DE Rat Protein P29067, SEQ ID NO 4052.
XX

KW Rat; Pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
OS Rattus norvegicus.
XX

PN WO2003016475-A2.
XX

PD 27-FEB-2003.
XX

PF 14-AUG-2002; 2002WO-US025765.
XX

PR 14-AUG-2001; 2001US-0312147P.
XX 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX

PA (GEHO) GEN HOSPITAL CORP.
(FARB) BAYER AG.
XX

PI Woolf C, D'urso D, Befort K, Costigan M;
XX

PS WPI; 2003-268312/26.
DR GENBANK; P29067.
XX

PT New composition preparing a medicament comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.

CC Claim 1; Page; 1017pp; English.

RESULT 16

ID ADE58182
XX ADE58182 standard; protein; 410 AA.

AC ADE58182;
XX

DT 29-JAN-2004 (first entry)
XX

DE Rat Protein P29067, SEQ ID NO 4052.
XX

KW Rat; Pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
OS Rattus norvegicus.
XX

PN WO2003016475-A2.
XX

PD 27-FEB-2003.
XX

PF 14-AUG-2002; 2002WO-US025765.
XX

PR 14-AUG-2001; 2001US-0312147P.
XX 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX

PA (GEHO) GEN HOSPITAL CORP.
(FARB) BAYER AG.
XX

PI Woolf C, D'urso D, Befort K, Costigan M;
XX

PS WPI; 2003-268312/26.
DR GENBANK; P29067.
XX

PT New composition preparing a medicament comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.

CC Claim 1; Page; 1017pp; English.

RESULT 17

ID ADE58183
XX ADE58183 standard; protein; 410 AA.

AC ADE58183;
XX

DT 29-JAN-2004 (first entry)
XX

DE Rat Protein P29067, SEQ ID NO 4052.
XX

KW Rat; Pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
OS Rattus norvegicus.
XX

PN WO2003016475-A2.
XX

PD 27-FEB-2003.
XX

PF 14-AUG-2002; 2002WO-US025765.
XX

PR 14-AUG-2001; 2001US-0312147P.
XX 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX

PA (GEHO) GEN HOSPITAL CORP.
(FARB) BAYER AG.
XX

PI Woolf C, D'urso D, Befort K, Costigan M;
XX

PS WPI; 2003-268312/26.
DR GENBANK; P29067.
XX

PT New composition preparing a medicament comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.

CC Claim 1; Page; 1017pp; English.

RESULT 18

ID ADE58184
XX ADE58184 standard; protein; 410 AA.

AC ADE58184;
XX

DT 29-JAN-2004 (first entry)
XX

DE Rat Protein P29067, SEQ ID NO 4052.
XX

KW Rat; Pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
OS Rattus norvegicus.
XX

PN WO2003016475-A2.
XX

PD 27-FEB-2003.
XX

PF 14-AUG-2002; 2002WO-US025765.
XX

PR 14-AUG-2001; 2001US-0312147P.
XX 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX

PA (GEHO) GEN HOSPITAL CORP.
(FARB) BAYER AG.
XX

PI Woolf C, D'urso D, Befort K, Costigan M;
XX

PS WPI; 2003-268312/26.
DR GENBANK; P29067.
XX

PT New composition preparing a medicament comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.

CC Claim 1; Page; 1017pp; English.

RESULT 19

ID ADE58185
XX ADE58185 standard; protein; 410 AA.

AC ADE58185;
XX

DT 29-JAN-2004 (first entry)
XX

DE Rat Protein P29067, SEQ ID NO 4052.
XX

KW Rat; Pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
OS Rattus norvegicus.
XX

PN WO2003016475-A2.
XX

PD 27-FEB-2003.
XX

PF 14-AUG-2002; 2002WO-US025765.
XX

PR 14-AUG-2001; 2001US-0312147P.
XX 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX

PA (GEHO) GEN HOSPITAL CORP.
(FARB) BAYER AG.
XX

PI Woolf C, D'urso D, Befort K, Costigan M;
XX

PS WPI; 2003-268312/26.
DR GENBANK; P29067.
XX

PT New composition preparing a medicament comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.

CC Claim 1; Page; 1017pp; English.

RESULT 20

ID ADE58186
XX ADE58186 standard; protein; 410 AA.

AC ADE58186;
XX

DT 29-JAN-2004 (first entry)
XX

DE Rat Protein P29067, SEQ ID NO 4052.
XX

KW Rat; Pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
OS Rattus norvegicus.
XX

PN WO2003016475-A2.
XX

PD 27-FEB-2003.
XX

PF 14-AUG-2002; 2002WO-US025765.
XX

PR 14-AUG-2001; 2001US-0312147P.
XX 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX

PA (GEHO) GEN HOSPITAL CORP.
(FARB) BAYER AG.
XX

PI Woolf C, D'urso D, Befort K, Costigan M;
XX

PS WPI; 2003-268312/26.
DR GENBANK; P29067.
XX

PT New composition preparing a medicament comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.

CC Claim 1; Page; 1017pp; English.

RESULT 21

ID ADE58187
XX ADE58187 standard; protein; 410 AA.

AC ADE58187;
XX

DT 29-JAN-2004 (first entry)
XX

DE Rat Protein P29067, SEQ ID NO 4052.
XX

KW Rat; Pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
OS Rattus norvegicus.
XX

PN WO2003016475-A2.
XX

PD 27-FEB-2003.
XX

PF 14-AUG-2002; 2002WO-US025765.
XX

PR 14-AUG-2001; 2001US-0312147P.
XX 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX

PA (GEHO) GEN HOSPITAL CORP.
(FARB) BAYER AG.
XX

PI Woolf C, D'urso D, Befort K, Costigan M;
XX

PS WPI; 2003-268312/26.
DR GENBANK; P29067.
XX

PT New composition preparing a medicament comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.

CC Claim 1; Page; 1017pp; English.

RESULT 22

ID ADE58188
XX ADE58188 standard; protein; 410 AA.

AC ADE58188;
XX

DT 29-JAN-2004 (first entry)
XX

DE Rat Protein P29067, SEQ ID NO 4052.
XX

KW Rat; Pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
OS Rattus norvegicus.
XX

PN WO2003016475-A2.
XX

PD 27-FEB-2003.
XX

CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp://wipo.int/pub/published_pct_sequences.

XX sequence 410 AA;

SQ

Query Match 2.9%; Score 11; DB 7; Length 410;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matched 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 341 ELPFVLMHPKP 351

Db 340 ELPFVLMHPKP 350

Search completed: February 9, 2005, 23:58:30

Job time : 166 sec

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OM protein - protein search, using sw model

Run on: February 9, 2005, 23:55:44 ; Search time 43 Seconds
 (without alignments)
 664.897 Million cell updates/sec

Title: Perfect score: US-10-056-405-2
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Scoring table: OLIGO Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	11	2.9	382	4 US-09-880-137-8
2	11	2.9	409	4 US-09-880-137-4
3	11	2.9	409	4 US-09-880-137-7
4	9	2.3	388	4 US-09-880-137-5
5	9	2.3	388	4 US-09-880-137-6
6	8	2.1	279	4 US-09-252-991A-27414
7	8	2.1	315	4 US-09-949-016-9940
8	8	2.1	401	4 US-09-949-016-8383
9	8	2.1	401	4 US-09-949-016-8384
10	8	2.1	410	4 US-09-880-137-3
11	8	2.1	418	4 US-09-880-137-1
12	8	2.1	418	4 US-09-880-137-2
13	7	1.8	15	2 US-08-484-905-28
14	7	1.8	15	3 US-08-481-985B-28
15	7	1.8	15	3 US-08-370-476-28
16	7	1.8	15	3 US-08-992-877-8
17	7	1.8	16	2 US-08-480-190-54
18	7	1.8	16	2 US-08-488-379-54
19	7	1.8	16	4 US-08-475-399A-54
20	7	1.8	16	4 US-08-077-255A-54
21	7	1.8	16	5 PCT-US93-07545-54
22	7	1.8	19	4 US-09-423-097-4
23	7	1.8	20	2 US-08-934-915-43
24	7	1.8	20	2 US-08-934-915-81
25	7	1.8	70	3 US-09-367-953B-29
26	7	1.8	70	3 US-09-367-953B-30
27	7	1.8	70	3 US-09-367-953B-30

RESULT 1
 US-09-880-137-8
 ; Sequence 8, Application US/09880137
 ; Patent No. 6640025
 ; GENERAL INFORMATION:
 APPLICANT: Bernstein, Gabriel
 TITLE OF INVENTION: METHODS OF ASSAYING FOR G LIGANDS AND MODULATORS
 FILE REFERENCE: MNI-131
 CURRENT APPLICATION NUMBER: US/09/880, 137
 CURRENT FILING DATE: 2001-03-05
 PRIOR APPLICATION NUMBER: US 60/186, 706
 PRIOR FILING DATE: 2000-03-03
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 8
 LENGTH: 382
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Homo sapiens mutation

RESULT 2
 US-09-880-137-4
 ; Sequence 4, Application US/09880137
 ; Patent No. 6640025
 ; GENERAL INFORMATION:
 APPLICANT: Bernstein, Gabriel
 TITLE OF INVENTION: METHODS OF ASSAYING FOR G LIGANDS AND MODULATORS
 FILE REFERENCE: MNI-131
 CURRENT APPLICATION NUMBER: US/09/880, 137
 CURRENT FILING DATE: 2001-03-05
 PRIOR APPLICATION NUMBER: US 60/186, 706
 PRIOR FILING DATE: 2000-03-03
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 4
 LENGTH: 409
 TYPE: PRT

; ORGANISM: Homo sapiens
US-09-880-137-4

Query Match

Best Local Similarity 2.9%; Score 11; DB 4; Length 409;

Matches 11; Conservative 100.0%; Pred. No. 0.03;

Mismatches 0; Indels 0; Gaps 0;

Qy 341 ELPFVLMPKP 351

Db 339 ELPFVLMPKP 349

RESULT 3

US-09-880-137-7

; Sequence 7, Application US/09880137

; Patent No. 6640025

; GENERAL INFORMATION:

; APPLICANT: Bernstein, Gabriel

; TITLE OF INVENTION: METHODS OF ASSAYING FOR G

; FILE REFERENCE: MNI-131

; CURRENT APPLICATION NUMBER: US/09/880,137

; PRIOR APPLICATION NUMBER: US 60/186,706

; CURRENT FILING DATE: 2000-03-03

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 7

; PRIORITY: 2001-03-05

; PRIOR FILING DATE: 2000-03-03

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 7

; PRIORITY: 2001-03-05

; PRIOR FILING DATE: 2000-03-03

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 7

; PRIORITY: 2001-03-05

; PRIOR FILING DATE: 2000-03-03

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 7

; PRIORITY: 2001-03-05

; PRIOR FILING DATE: 2000-03-03

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 7

; PRIORITY: 2001-03-05

; PRIOR FILING DATE: 2000-03-03

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 7

; PRIORITY: 2001-03-05

; PRIOR FILING DATE: 2000-03-03

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 7

US-09-880-137-7

OTHER INFORMATION: Description of Artificial Sequence: Homo sapiens mutation

Query Match

Best Local Similarity 2.9%; Score 11; DB 4; Length 409;

Matches 11; Conservative 100.0%; Pred. No. 0.03;

Mismatches 0; Indels 0; Gaps 0;

Qy 341 ELPFVLMPKP 351

Db 339 ELPFVLMPKP 349

RESULT 4

US-09-880-137-5

; Sequence 5, Application US/09880137

; Patent No. 6640025

; GENERAL INFORMATION:

; APPLICANT: Bernstein, Gabriel

; TITLE OF INVENTION: METHODS OF ASSAYING FOR G

; FILE REFERENCE: MNI-131

; CURRENT APPLICATION NUMBER: US/09/252,991A

; PRIOR APPLICATION NUMBER: US 60/094,190

; CURRENT FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 27414

; LENGTH: 279

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-880-137-5

Query Match

Best Local Similarity 2.3%; Score 9; DB 4; Length 388;

Matches 9; Conservative 100.0%; Pred. No. 2.5;

Mismatches 0; Indels 0; Gaps 0;

Qy 22 GKRDFVFDHV 30

Db 19 GKRDFVFDHV 27

; Sequence 7, Application US/09880137

; Patent No. 6640025

; GENERAL INFORMATION:

; APPLICANT: Venter, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: CLO01307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

RESULT 5

US-09-880-137-6

; Sequence 6, Application US/09880137

; Patent No. 6640025

; GENERAL INFORMATION:

; APPLICANT: Bernstein, Gabriel

; TITLE OF INVENTION: METHODS OF ASSAYING FOR G

; FILE REFERENCE: MNI-131

; CURRENT APPLICATION NUMBER: US/09/880,137

; PRIOR APPLICATION NUMBER: US 60/186,706

; CURRENT FILING DATE: 2000-03-03

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 6

; LENGTH: 388

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-880-137-6

Query Match

Best Local Similarity 2.3%; Score 9; DB 4; Length 388;

Matches 9; Conservative 100.0%; Pred. No. 2.5;

Mismatches 0; Indels 0; Gaps 0;

Qy 22 GKRDFVFDHV 30

Db 19 GKRDFVFDHV 27

; Sequence 7, Application US/09880137

; Patent No. 6640025

; GENERAL INFORMATION:

; APPLICANT: Venter, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: CLO01307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

RESULT 6

US-09-252-991A-27414

; Sequence 27414, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenstein et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE REFERENCE: 107196-136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 27414

; LENGTH: 279

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-27414

Query Match

Best Local Similarity 2.1%; Score 8; DB 4; Length 279;

Matches 8; Conservative 100.0%; Pred. No. 17;

Mismatches 0; Indels 0; Gaps 0;

Qy 336 GELSAELP 343

Db 30 GELSAELP 37

; Sequence 9940, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: Venter, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: CLO01307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

RESULT 7

US-09-949-016-9940

; Sequence 9940, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: Venter, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: CLO01307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

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; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9940
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-9940

Query Match          2.1%; Score 8; DB 4; Length 315;
Best Local Similarity 100.0%; Pred. No. 20; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
US-09-949-016-8383
; Sequence 8383, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SEQ ID NO 8383
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-8383

Query Match          2.1%; Score 8; DB 4; Length 401;
Best Local Similarity 100.0%; Pred. No. 24; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 10
US-09-880-137-3
; Sequence 3, Application US/09880137
; Patent No. 6640025
; GENERAL INFORMATION:
; APPLICANT: Bernstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
; FILE REFERENCE: MNI-131
; CURRENT APPLICATION NUMBER: US/09/880,137
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-880-137-3

Query Match          2.1%; Score 8; DB 4; Length 410;
Best Local Similarity 100.0%; Pred. No. 25; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 9
US-09-949-016-8384
; Sequence 8384, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; SEQ ID NO 1
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Bos taurus
; US-09-880-137-1

Query Match          2.1%; Score 8; DB 4; Length 418;
Best Local Similarity 100.0%; Pred. No. 25; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy

22 GKRDVFVDH 29

||||||| 30

Db

23 GKRDVFVDH 30

RESULT 12

US-09-880-137-2

; Sequence 2, Application US/09880137

; Patent No. 6640025

; GENERAL INFORMATION:

; APPLICANT: Bernstein, Gabriel

; TITLE OF INVENTION: METHODS OF ASSAYING FOR G

; FILE REFERENCE: MNI-131

; CURRENT APPLICATION NUMBER: US/09/880,137

; CURRENT FILING DATE: 2001-03-05

; PRIOR APPLICATION NUMBER: US 60/186,706

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PastSEQ for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 418

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-880-137-2

Query Match

Best Local Similarity 2.1%; Score 8; DB 4; Length 418;

; Matches 8; Conservative 100.0%; Pred. No. 25;

; Mismatches 0; Indels 0; Gaps 0;

Qy 22 GKRDVFVDH 29

Db 23 GKRDVFVDH 30

RESULT 13

US-08-484-905-28

; Sequence 28, Application US/08484905

; Patent No. 5976551

; GENERAL INFORMATION:

; APPLICANT: Mottez, Estelle

; APPLICANT: Abastado, Jean-Pierre

; APPLICANT: Kourilsky, Philippe

; TITLE OF INVENTION: An Altered Major Histocompatibility

; TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the

; NUMBER OF SEQUENCES: 127

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

; STREET: 1300 I Street, N.W., Suite 700

; CITY: Washington

; STATE: D.C.

; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/481,985B

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/792,473

; FILING DATE: 15-NOV-1991

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/801,818

; FILING DATE: 05-DEC-1991

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/792,473

; FILING DATE: 15-NOV-1991

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Potter, Jane E. R.

RESULT 14

US-08-481-985B-28

; Sequence 28, Application US/08481985B

; Patent No. 6011146

; GENERAL INFORMATION:

; APPLICANT: Mottez, Estelle

; APPLICANT: Abastado, Jean-Pierre

; APPLICANT: Kourilsky, Philippe

; TITLE OF INVENTION: Altered Major Histocompatibility Complex

; NUMBER OF SEQUENCES: 148

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

; STREET: 1300 I Street, N.W., Suite 700

; CITY: Washington

; STATE: D.C.

; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US 07/801,818

; FILING DATE: 05-DEC-1991

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/792,473

; FILING DATE: 15-NOV-1991

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Meyers, Kenneth J.

; REGISTRATION NUMBER: 25,146

; REFERENCE/DOCKET NUMBER: 03495.0106-04000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-408-4000

; TELEFAX: 202-408-4400

; INFORMATION FOR SEQ ID NO:

; SEQUENCE CHARACTERISTICS: 28:

; LENGTH: 15 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-481-985B-28

; Query Match

Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: February 10, 2005, 00:11:11
 Job time : 44 secs

Qy 256 LETSEGC 262
 Db 1 LETSEGC 7

RESULT 15
 US-08-370-476-28
 Sequence 28, Application US/08370476

Patent No. 6153408

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GENERAL INFORMATION:
 APPLICANT: Mottez, Estelle
 APPLICANT: Abastado, Jean-Pierre
 APPLICANT: Kourilsky, Phillippe
 APPLICANT: Lone, Yu-Chun
 APPLICANT: Ojcius, David
 APPLICANT: Cabrouge, Arminda
 TITLE OF INVENTION: Altered Major Histocompatibility Complex

NUMBER OF SEQUENCES: 127

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Finnegan, Henderson, Parabow, Garrett &

STREET: 1300 I Street, N.W., Suite 700

CITY: Washington

STATE: D.C.

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/370,476

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/117,575

FILING DATE: 07-SEP-1993

APPLICATION NUMBER: US 08/072,787

FILING DATE: 06-JUN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/801,818

FILING DATE: 05-DEC-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/792,473

FILING DATE: 15-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Kenneth J.

REGISTRATION NUMBER: 25,146

REFERENCE/DOCKET NUMBER: 05243.0001-01000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-370-476-28

Query Match 1.8%; Score 7; DB 3; Length 15;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 256 LETSEGC 262
 Db 1 LETSEGC 7

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OM protein - protein search, using sw model

Run on:

February 9, 2005, 23:58:40 ; Search time 131 Seconds

(without alignments)
952.245 Million cell updates/sec

Title: US-10-056-405-2
Perfect score: 383
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Scoring table: Oligo Gapop 60.0 , Gapext 60.0
Searched: 1373511 seqs, 325702437 residues
Word size : 0
Total number of hits satisfying chosen parameters: 1373511
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Listing first 45 summaries

Database :

1: Published Applications AA: *
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 3: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1
US-10-094-240-2
; Sequence 2, Application US/10094240
; Publication No. US20030082637A1
; GENERAL INFORMATION:
; APPLICANT: ZWIEBEL, LAURENCE J.
; TITLE OF INVENTION: ARRESTIN GENE, POLYPEPTIDE, AND METHODS OF USE THEREOF
; FILE REFERENCE: N8289
; CURRENT APPLICATION NUMBER: US/10/094,240
; CURRENT FILING DATE: 2001-03-08
; PRIORITY NUMBER: 10/056,405
; PRIORITY FILING DATE: 2002-01-24
; PRIORITY APPLICATION NUMBER: 60/264,649
; PRIORITY FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Anopheles gambiae
; us-10-094-240-2

Query Match 100.0%; Score 383; DB 14; Length 383;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MVYNFKVKKKCARNGVLY.....ADVETFRQDTIDQQASVDFE 60

Qy 61 FRYGREGEDVMGLNFOKEKLCLASEQIYPRPEKSDEKEQTKLQERLLKKLGNSNAIPFTNIS 120
Db 61 FRYGREGEDVMGLNFOKEKLCLASEQIYPRPEKSDEKEQTKLQERLLKKLGNSNAIPFTNIS 120

Qy 121 PNAPSSVTLQQGEDDNGDPGCVSYVVKFAGESETDRTHRSTVTLIGRKIOPFKTQGQ 180

CURRENT FILING DATE: 2001-03-08
 PRIOR APPLICATION NUMBER: 10/056,405
 PRIOR FILING DATE: 2002-01-24
 PRIOR APPLICATION NUMBER: 60/264,649
 NUMBER OF SEQ ID NOS: 27
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 25
 LENGTH: 398
 TYPE: PRT
 ORGANISM: *Anopheles gambiae*
 US-10-094-240-25

RESULT 6
 Query Match 2.9%; Score 11; DB 14; Length 398;
 Best Local Similarity 100.0%; Pred. No. 0.11; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 62 RYGREEDEVMG 72
 Db 61 RYGREEDEVMG 71

RESULT 6
 US-10-094-240-27
 Sequence 27, Application US/10094240
 Publication No. US20030082637A1
 GENERAL INFORMATION:
 APPLICANT: ZWIEBEL, LAURENCE J.
 TITLE OF INVENTION: ARRESTIN GENE, POLYPEPTIDE, AND METHODS OF USE THEREOF
 FILE REFERENCE: NB289
 CURRENT APPLICATION NUMBER: US/10/094, 240
 CURRENT FILING DATE: 2001-03-08
 PRIOR APPLICATION NUMBER: 10/056, 405
 PRIOR FILING DATE: 2002-01-24
 PRIOR APPLICATION NUMBER: 60/264, 649
 PRIOR FILING DATE: 2001-01-26
 NUMBER OF SEQ ID NOS: 27
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 27
 LENGTH: 401
 TYPE: PRT
 ORGANISM: *Drosophila melanogaster*
 US-10-094-240-27

Query Match 2.9%; Score 11; DB 14; Length 401;
 Best Local Similarity 100.0%; Pred. No. 0.1; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 62 RYGREEDEVMG 72
 Db 61 RYGREEDEVMG 71

RESULT 7
 US-09-880-137-4
 Sequence 4, Application US/09880137
 Publication No. US20020031295A1
 GENERAL INFORMATION:
 APPLICANT: Bernstein, Gabriel
 TITLE OF INVENTION: METHODS OF ASSAYING FOR G PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
 FILE REFERENCE: MNI-131
 CURRENT APPLICATION NUMBER: US/09/800, 137A
 CURRENT FILING DATE: 2001-03-05
 PRIOR APPLICATION NUMBER: US 60/186, 706
 PRIOR FILING DATE: 2000-03-03
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 4
 LENGTH: 409
 TYPE: PRT
 ORGANISM: *Homo sapiens*
 US-09-800-137A-4

Query Match 2.9%; Score 11; DB 10; Length 409;
 Best Local Similarity 100.0%; Pred. No. 0.11; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 341 ELPFVLMHPKP 351
 Db 339 ELPFVLMHPKP 349

RESULT 8
 US-09-880-137-7
 Sequence 7, Application US/09880137
 Patent No. US20020031295A1
 GENERAL INFORMATION:
 APPLICANT: Bernstein, Gabriel
 TITLE OF INVENTION: METHODS OF ASSAYING FOR G PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
 FILE REFERENCE: MNI-131
 CURRENT APPLICATION NUMBER: US/09/880, 137
 CURRENT FILING DATE: 2001-03-05
 PRIOR APPLICATION NUMBER: US 60/186, 706
 PRIOR FILING DATE: 2000-03-03
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 4
 LENGTH: 409
 TYPE: PRT
 ORGANISM: *Homo sapiens*
 US-09-880-137-4

RESULT 10

US-09-800-137A-7
; Sequence 7, Application US/09800137A
; Publication No. US2003015753A1
; GENERAL INFORMATION:
; APPLICANT: Bernstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
; FILE REFERENCE: JHV-028.01
; CURRENT APPLICATION NUMBER: US/10/722,357
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: 60/413,152
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 09/800,137A
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 7
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Homo sapiens mutation
US-09-800-137A-7
Query Match
Best Local Similarity 2.9%; Score 11; DB 10; Length 409;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 341 ELPFVLMHPKP 351
Db 339 ELPFVLMHPKP 349

RESULT 11
US-10-038-010-54
; Sequence 54, Application US/10038010
; Publication No. US20030040089A1
; GENERAL INFORMATION:
; APPLICANT: HYBRIGENICS
; APPLICANT: Pierre, Legrain
; TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
; FILE REFERENCE: B4767A
; CURRENT APPLICATION NUMBER: US/10/038,010
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 60/259,377
; PRIOR FILING DATE: 2001-01-02
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: beta Arrestin2
; LOCATION: (1)..(410)
; OTHER INFORMATION:
US-10-038-010-54

Query Match
Best Local Similarity 100.0%; Score 11; DB 14; Length 410;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 341 ELPFVLMHPKP 351
Db 340 ELPFVLMHPKP 350

RESULT 12
US-10-722-357-31
; Sequence 31, Application US/10722357
; Publication No. US20040191803A1
; GENERAL INFORMATION:
; APPLICANT: GALLAGHER, MICHELA
; APPLICANT: LUND, PAULINE KAY
; APPLICANT: ROTHSTEIN, JEFFREY

Query Match
Best Local Similarity 2.9%; Score 11; DB 16; Length 466;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 341 ELPFVLMHPKP 351
Db 349 ELPFVLMHPKP 406

RESULT 13
US-09-880-137-5
; Sequence 5, Application US/09880137
; Patent No. US20020031295A1
; GENERAL INFORMATION:
; APPLICANT: Bernstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
; FILE REFERENCE: JHV-028.01
; CURRENT APPLICATION NUMBER: US/10/722,357
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: 60/413,152
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 09/800,137A
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-137-5

Query Match
Best Local Similarity 2.3%; Score 9; DB 9; Length 388;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 22 GKRDFDVHV 30
Db 19 GKRDFDVHV 27

RESULT 14
US-09-880-137-6
; Sequence 6, Application US/09880137
; Patent No. US20020031295A1
; GENERAL INFORMATION:
; APPLICANT: Bernstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
; FILE REFERENCE: JHV-028.01
; CURRENT APPLICATION NUMBER: US/10/722,357
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: 60/413,152
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-137-6

Query Match 2.3%; Score 9; DB 9; Best Local Similarity 100.0%; Pred. No. 8.3; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 22 GKRDFVHV 30
Db 19 GKRDFVHV 27

RESULT 15
US-09-800-137A-5
; Sequence 5, Application US/09800137A
; Publication No. US20030157553A1
; GENERAL INFORMATION:
; APPLICANT: Bernstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
; FILE REFERENCE: MNI-131
; CURRENT APPLICATION NUMBER: US/09/800,137A
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-800-137A-5

Query Match 2.3%; Score 9; DB 10; Length 388;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 22 GKRDFVHV 30
Db 19 GKRDFVHV 27

Search completed: February 10, 2005, 00:13:29
Job time : 132 sec

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Qy	121		PNAPSSVTLQQGEDDNGDPGVSYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQ	Qy	181		QPCCTLVRKDFMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKMKKKIKAMVQGVD
Db	121		PNAPSSVTLQQGEDDNGDPGVSYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQ	Db	215		QPCCTLVRKDFMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKMKKKIKAMVQGVD
Qy	181		QPCCTLVRKDFMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKMKKKIKAMVQGVD	Qy	240		QPCCTLVRKDFMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKMKKKIKAMVQGVD
Db	181		QPCCTLVRKDFMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKMKKKIKAMVQGVD	Db	240		QPCCTLVRKDFMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKMKKKIKAMVQGVD
Qy	241		VVLFONGSYRNVTASLETSEGCP1QPGSSLQKVNMLTPLLSNKKRGGIAALDGQIKRQDO	Qy	241		VVLFONGSYRNVTASLETSEGCP1QPGSSLQKVNMLTPLLSNKKRGGIAALDGQIKRQDO
Db	241		VVLFONGSYRNVTASLETSEGCP1QPGSSLQKVNMLTPLLSNKKRGGIAALDGQIKRQDO	Db	240		VVLFONGSYRNVTASLETSEGCP1QPGSSLQKVNMLTPLLSNKKRGGIAALDGQIKRQDO
Qy	301		CLASTILLAQPQDQDAFGVIVISYAVKVLFLGALGGELSAELPFWLMHPKPGTKAVIHA	Qy	300		CLASTILLAQPQDQDAFGVIVISYAVKVLFLGALGGELSAELPFWLMHPKPGTKAVIHA
Db	301		CLASTILLAQPQDQDAFGVIVISYAVKVLFLGALGGELSAELPFWLMHPKPGTKAVIHA	Db	360		CLASTILLAQPQDQDAFGVIVISYAVKVLFLGALGGELSAELPFWLMHPKPGTKAVIHA
Qy	361		DSQADVETFRQTDQOQASVDFE 383	Qy	361		DSQADVETFRQTDQOQASVDFE 383
Db	361		DSQADVETFRQTDQOQASVDFE 383	Db	395		DSQADVETFRQTDQOQASVDFE 417
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ID	Q7PMG5	PRELIMINARY;	PRT;	417 AA.	ID	Q6VPP0	PRELIMINARY;
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DT	01-MAR-2004	(TREMBLrel. 26, Created)			DT	05-JUL-2004	(TREMBLrel. 27, Created)
DT	01-MAR-2004	(TREMBLrel. 26, Last sequence update)			DT	05-JUL-2004	(TREMBLrel. 27, Last sequence update)
DE	ENSANGP0000012569	(Fragment).			DE	Arrestin (Fragment).	
GN	Name=ENSANGG0000010080;				OS	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.	
OS	Anopheles gambiae str. PEST.				OC	Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.	
OC	Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.				OC	NCBI_TaxID=7165;	
RN	[1]				RN	[1]	
RR	SEQUENCE FROM N.A.				RR	SEQUENCE FROM N.A.	
RA	STRAIN=PEST;				RA	STRAIN=4aRR, Yaounde, and L3-5;	
RL	Anopheles Genome Sequencing Consortium;				RL	Morlais I., Poncon N., Simard F., Cohuet A., Fontenille D.;	
CC	Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.				RL	Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.	
CC	- - CAUTION: The sequence shown here is derived from an				DR	EMBL; AY333991; AAR0116.1; -.	
CC	preliminary data. The sequence shown here is derived from an				DR	EMBL; AY333992; AAR0117.1; -.	
CC	preliminary data. The sequence shown here is derived from an				DR	EMBL; AY333993; AAR0118.1; -.	
CC	preliminary data. The sequence shown here is derived from an				DR	EMBL; AY333990; AAR0115.1; -.	
DR	EMBL; AY333994; AAR0111.1; -.				DR	EMBL; AY333996; AAR0112.1; -.	
DR	HSSP; P17870; 14M.				DR	EMBL; AY333994; AAR0119.1; -.	
DR	HSSP; P17870; 14M.				DR	HSSP; P08168; 1AYR.	
DR	GO; GO:0007600; P:sensory perception; IEA.				DR	GO; GO:0007600; P:sensory perception; IEA.	
DR	GO; GO:0007165; P:signal transduction; IEA.				DR	GO; GO:0007165; P:signal transduction; IEA.	
DR	InterPro; IPR000698; Arrestin.				DR	InterPro; IPR000698; Arrestin.	
DR	InterPro; IPR011022; Arrestin_C.				DR	InterPro; IPR011022; Arrestin_C.	
DR	InterPro; IPR011021; Arrestin_N.				DR	InterPro; IPR011021; Arrestin_N.	
DR	Pfam; PF02752; Arrestin_C; 1.				DR	Pfam; PF00339; Arrestin_N; 1.	
DR	Pfam; PF00339; Arrestin_N; 1.				DR	PRINTS; PR00309; ARRESTIN.	
DR	PRINTS; PR00309; ARRESTIN.				DR	PRINTS; PR00309; ARRESTIN.	
DR	ProDom; PD002099; Arrestin; 2.				DR	ProDom; PD002099; Arrestin; 2.	
DR	PROSITE; PS00295; ARRESTINS; 1.				FT	NON_TER 1 1	
FT	NON_TER 1 1				FT	NON_TER 1 1	
SQ	SEQUENCE 417 AA; 46591 MW; 4EE98A3C3225FC0 CRC64;				SQ	SEQUENCE 245 AA; 27038 MW; 86D8F4520115DA5F CRC64;	
Query Match	100.0%; Score 383; DB 2; Length 417;				Query Match	64.0%; Score 245; DB 2; Length 245;	
Best Local Similarity	100.0%; Pred. No. 0;				Best Local Similarity	100.0%; Pred. No. 1.3e-236;	
Matches	383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				Matches	245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1		MYVNFKVFKKCAPNGKVTLYMGKRDVFVHDVSGVEPIGIVVLDPEYIRDNRKVFQIVCS	Qy	129		QPCCTLVRKDFMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKMKKKIKAMVQGVD
Db	35		MYVNFKVFKKCAPNGKVTLYMGKRDVFVHDVSGVEPIGIVVLDPEYIRDNRKVFQIVCS	Db	1		QPCCTLVRKDFMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKMKKKIKAMVQGVD
Qy	61		FRYGRGEEDEVMLNFOKELCLASEQIYPRPEKSDEQTKLQERLKKLGSNAIPFTFNIS	Qy	189		QPCCTLVRKDFMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKMKKKIKAMVQGVD
Db	95		FRYGRGEEDEVMLNFOKELCLASEQIYPRPEKSDEQTKLQERLKKLGSNAIPFTFNIS	Db	61		QPCCTLVRKDFMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKMKKKIKAMVQGVD
Qy	121		PNAPSSVTLQQGEDDNGDPGVSYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQ	Qy	249		QPCCTLVRKDFMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKMKKKIKAMVQGVD
Db	121		PNAPSSVTLQQGEDDNGDPGVSYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQ	Db	121		QPCCTLVRKDFMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKMKKKIKAMVQGVD
Qy	180		PNAPSSVTLQQGEDDNGDPGVSYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQ	Qy	180		QPCCTLVRKDFMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNKMKKKIKAMVQGVD

RX MEDLINE=91282780; PubMed=1905538;
 RA Matsumoto H., Yamada T.;
 RT "Phosrestins I and II: arrestin homologs which undergo differential
 light-induced phosphorylation in the *Drosophila* photoreceptor *in
 vivo*.";
 RL Biochem. Biophys. Res. Commun. 177:1306-1312(1991).
 RN [7]
 RP FUNCTION.
 RX MEDLINE=93303590; PubMed=8316831;
 RA Dolph P.J., Ranganathan R., Colley N.J., Hardy R.W., Socolich M.,
 Zuker C.S.;
 RT "Arrestin function in inactivation of G protein-coupled receptor
 rhodopsin *in vivo*";
 RL Science 260:1910-1916(1993).
 CC -!- FUNCTION: Regulates photoreceptor cell deactivation. Arr1 and Arr2
 proteins are mediators of rhodopsin inactivation and are essential
 for the termination of the phototransduction cascade.
 CC -!- TISSUE SPECIFICITY: Expressed specifically and abundantly in the
 photoreceptors. Inner and outer segments, and the inner plexiform
 regions of the retina.
 CC -!- PTM: Phosphorylated, but does not undergo light-induced
 phosphorylation.
 CC -!- SIMILARITY: Belongs to the arrestin family.
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 CC
 DR EMBL; M30177; -; NOT_ANNOTATED_CDS.
 DR EMBL; M30140; AAA28380.1; -.
 DR EMBL; AE003657; AA553644.1; -.
 DR EMBL; AY061824; AAU27635.1; -.
 DR PIR; A34867; A34867.
 DR HSSP; P17870; 1G4M.
 DR IntAct; P15372; -.
 DR FlyBase; FBgn0000120; Arr1.
 DR GO; GO:0005624; C:membrane fraction; IDA.
 DR GO; GO:0016028; C:rhabdomere; IDA.
 DR InterPro; IPR00698; Arrestin.
 DR InterPro; IPR011022; Arrestin_C.
 DR Pfam; PF02752; Arrestin_C; 1.
 DR Pfam; PF00339; Arrestin_N; 1.
 DR PRINTS; PR00309; ARRESTIN.
 DR Prodom; PD00209; Arrestin; 2.
 DR PROSITE; PS00295; ARRESTINS; 1.
 KW Phosphorylation; Sensory transduction; Vision.
 SQ SEQUENCE 364 AA; 40771 MW; 0DCC764C4F890FC2 CRC64;
 Query Match 5.2%; Score 20; DB 1; Length 364;
 Best Local Similarity 100.0%; Pred. No. 5.8e-11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 AC QY 228 VKKIKAMVQOGDVWLFGONG 247
 DB 227 VKKIKAMVQOGDVWLFGONG 246
 RESULT 6
 Q7YTV9 PRELIMINARY; PRT; 18 AA.
 ID Q7YTV9
 AC Q7YTV9;
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DE Arrestin (Fragment).
 GN Name=arr1;
 OS Anopheles stephensi (Indo-Pakistan malaria mosquito).
 OS Anopheles stephensi (Indo-Pakistan malaria mosquito).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
 OC NCBI_TaxID=30069;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Favio G., ricci I., Casiraghi M., Esposito F.;
 RL Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
 FT EMBL; AJ544226; CAD66651.1; -.
 SQ SEQUENCE 18 AA; 18 MW; A273A394A2A6EF66 CRC64;
 Query Match 4.7%; Score 18; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.6e-10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 AC QY 1 MVYNFKVFKKCAPNGKVT 18
 DB 1 MVYNFKVFKKCAPNGKVT 18
 SQ SEQUENCE FROM N.A.
 RA Favio G., ricci I., Casiraghi M., Esposito F.;
 RL Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
 FT EMBL; AJ544225; CAD66650.1; -.
 SQ SEQUENCE FROM N.A.
 RA Favio G., ricci I., Casiraghi M., Esposito F.;
 RL Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AJ544225; CAD66650.1; -.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Favio G., ricci I., Casiraghi M., Esposito F.;
 RL Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AJ544224; CAD66649.1; -.
 FT NON_TER 18 18
 SQ SEQUENCE 18 AA; 2075 MW; A273A394A2A6EF66 CRC64;
 Query Match 4.7%; Score 18; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.6e-10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 AC QY 1 MVYNFKVFKKCAPNGKVT 18
 DB 1 MVYNFKVFKKCAPNGKVT 18
 SQ SEQUENCE 18 AA; 2075 MW; A273A394A2A6EF66 CRC64;
 Query Match 4.7%; Score 18; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.6e-10;

DT 01-OCT-1995 (Rel. 34, Created)
 DT 01-OCT-1995 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Arrestin, lateral eye.
 OS Limulus polyphemus (Atlantic horseshoe crab).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
 OC Limulidae; Limulus.
 NCBI_TaxID=6850;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Retina;
 RX MEDLINE=95096819; PubMed=7798902;
 RA Smith W.C., Greenberg R.M., Calman B.G., Hendrix M.M., Hutchinson L.,
 DR Donoso L.A., Battelle B.-A.;
 RT "Isolation and expression of an arrestin cDNA from the horseshoe crab
 lateral eye.";
 RL J. Neurochem. 64:1-13 (1995).
 CC -!- FUNCTION: Plays an important role in the photoreceptor
 CC transduction.
 CC -!- PTM: Phosphorylated.
 CC -!- SIMILARITY: Belongs to the arrestin family.
 CC
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 CC
 DR EMBL; S57174; AAB25860.1; -.
 DR PIR; A56607; A56607.
 DR HSSP; P17870; 1G4M.
 DR InterPro; IPR00698; Arrestin.
 DR InterPro; IPR011022; Arrestin_C.
 DR InterPro; IPR011021; Arrestin_N.
 DR Pfam; PF02752; Arrestin_C; 1.
 DR Pfam; PF02752; Arrestin_N; 1.
 DR PRINTS; PR00339; ARRESTIN.
 DR PRODOM; PD002099; Arrestin; 2.
 DR PROSITE; PS00295; ARRESTINS; 1.
 DR KW Sensory transduction.
 DR SQ SEQUENCE 407 AA; 45543 MW; DEC28A3A534935BB CRC64;
 DR Query Match 3.1%; Score 12; DB 1; Length 407;
 DR Best Local Similarity 100.0%; Pred. No. 0.0057;
 DR Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DR Qy 62 RYGRGEEDEVWGL 73
 DR Db 69 RYGRGEEDEVWGL 80
 DR
 DR InterPro; IPR011022; Arrestin_C.
 DR InterPro; IPR011021; Arrestin_N.
 DR Pfam; PF02752; Arrestin_C; 1.
 DR PRINTS; PR00339; ARRESTIN.
 DR PRODOM; PD002099; Arrestin; 2.
 DR PROSITE; PS00295; ARRESTINS; 1.
 DR KW Phosphorylation; Sensory transduction; Vision.
 DR SQ SEQUENCE 400 AA; 44302 MW; F30D0D25BC2BEE33 CRC64;
 DR Query Match 3.4%; Score 13; DB 1; Length 400;
 DR Best Local Similarity 100.0%; Pred. No. 0.0065;
 DR Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DR Qy 61 FRYGGREEDEVWGL 73
 DR Db 68 FRYGGREEDEVWGL 80
 DR
 DR RESULT 13
 DR ARRH_LOCMI STANDARD; PRT; 407 AA.
 DR ID ARRH_LOCMI
 DR AC P32122;
 DR DT 01-OCT-1993 (Rel. 27, Created)
 DR DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DR DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DR DE Arrestin homolog.
 DR OS Locusta migratoria (Migratory locust).
 DR OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 DR OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acrididae;
 DR OC Acridoidea; Acrididae; Oedipodinae; Locusta.
 DR NCBI_TaxID=7004;
 DR RN [1]
 DR RP SEQUENCE FROM N.A.
 DR RC TISSUE=Antenna;
 DR RX MEDLINE=9319955; PubMed=8452755; DOI=10.1016/0898-6568(93)90009-B;
 DR Raming K., Freitag J., Krieger J., Breer H.;
 DR "Arrestin-subtypes in insect antennae.";
 DR Cell. Signal. 5:69-80(1993).
 DR CC -!- SIMILARITY: Belongs to the arrestin family.
 DR
 DR RESULT 14
 DR O68DZ5 PRELIMINARY; PRT; 217 AA.
 DR ID Q68DZ5
 DR AC Q68DZ5;
 DR DT 25-OCT-2004 (TREMBLrel. 28, Created)
 DR DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DR DE Hypothetical protein DKFZp686L0365.
 DR GN Name=DKFZp686L0365;
 DR OS Homo sapiens (Human).
 DR OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 DR OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 DR RN [1]
 DR RP SEQUENCE FROM N.A.
 DR RG The German cDNA Consortium;
 DR RA Ottewaelder B., Obermaier B., Deutscherbaur S., Schaiapp A., Wiemann S.;
 DR Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
 DR RL Submitted (AUG 2004) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; CR749218; CAH18075.1; -.
 DR InterPro; IPR00698; Arrestin.
 DR InterPro; IPR011022; Arrestin_C.
 DR Pfam; PF02752; Arrestin_C; 1.
 DR PRODOM; PD002099; Arrestin; 1.
 DR DR KW Hypothetical protein.
 DR SQ SEQUENCE 217 AA; 24362 MW; 61653F5BACBB0FD CRC64;
 DR Query Match 2.9%; Score 11; DB 2; Length 217;
 DR Best Local Similarity 100.0%; Pred. No. 0.039;
 DR Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DR Qy 341 ELPPFVLMHPKP 351
 DR Db 147 ELPPFVLMHPKP 157
 DR
 DR RESULT 15
 DR Q66GU6 PRELIMINARY; PRT; 398 AA.
 DR AC Q66GU6;

DT 25-OCT-2004 (TREMBLrel. 28, Created)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Arrestin 2-like protein Arr2.
 GN Name=ARR2;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
 OX NCBI_TaxID=180454;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=PEST;
 RX MEDLINE=23159591; PubMed=14986925;
 RA Merrill C.E., Pitts R.J., Zwiebel L.J.;
 RT "Molecular characterization of arrestin family members in the malaria
 vector mosquito, *Anopheles gambiae*.",
 RL Insect Mol. Biol. 12:641-650(2003).
 DR EMBL; BK000996; DAA0088.1; -.
 DR InterPro; IPR00698; Arrestin.
 DR InterPro; IPR011022; Arrestin_C.
 DR InterPro; IPR011021; Arrestin_N.
 DR Pfam; PF02752; Arrestin_C; 1.
 DR Pfam; PF00339; Arrestin_N; 1.
 DR PRINTS; PR00309; ARRESTIN.
 DR ProDom; PD002099; Arrestin; 2.
 DR PROSITE; PS00295; ARRESTINS; 1.
 DR SEQUENCE 398 AA; 44536 MW; 73DD73FB34F01418 CRC64;
 Query Match 2.9%; Score 11; DB 2; Length 398;
 Best Local Similarity 100.0%; Pred. No. 0.066;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 62 RYGRGEEDEVMG 72
 Db 61 RYGRGEEDEVMG 71

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 Job time : 177 secs

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